142526

From:	Chan, Christina
Sent:	Wednesday, January 12, 2005 6:55 PM
To:	Ramirez, Delia; STIC-Biotech/ChemLib
Subject:	RE: rush search 09/965825

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Ramirez, Delia
Sent: Wednesday, January 12, 2005 6:25 PM
To: Chan, Christina
Subject: rush search 09/965825

Hi Christina,

Please approve the following interference search: seq id no: 1, 4 and 2 in the nucleic acid databases.

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

GenCore version 5.1.6

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Run on: January 15, 2005, 07:17:41 ; Search time 254.651 Seconds

OM nucleic - nucleic search, using sw model

9065.911 Million cell updates/sec
(without alignments)

Title: US-09-965-825-4
Perfect score: 3248
Sequence: 1 gctctcgcagcaacaagagc..............tggcaatgacggtgtgtctct 3248

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length DB	ID	Description
1	366.2	11.3	1746	4	US-09-543-681A-4139	Sequence 4139, Ap
2	362.8	11.2	1749	4	US-09-489-039A-4884	Sequence 4884, Ap
3	305.2	9.4	1719	4	US-09-231-818-6	Sequence 6, Appli
4	269.4	8.3	1737	4	US-10-096-571-1	Sequence 1, Appli
5	227.4	7.0	1293	4	US-09-252-991A-7335	Sequence 7335, Ap
6	164.2	5.1	1083	4	US-09-489-039A-4905	Sequence 4905, Ap
7	164.2	5.1	1113	4	US-09-252-991A-7413	Sequence 7413, Ap
8	155	4.8	1454	4	US-09-252-991A-7281	Sequence 7281, Ap
9	152.8	4.7	1448	4	US-10-096-571-7	Sequence 7, Appli
10	152.8	4.7	7900	4	US-10-096-571-8	Sequence 8, Appli
11	138.8	4.3	7900	4	US-08-956-171B-138	Sequence 138, App
12	138.8	4.3	798	4	US-08-781-986A-138	Sequence 138, App
13	129.6	4.0	1746	4	US-09-252-991A-7166	Sequence 7166, Ap
14	110.2	3.4	1761	3	US-09-107-532A-3181	Sequence 3181, Ap
15	101.6	3.1	2577	4	US-09-134-001C-1619	Sequence 1619, Ap
16	100.4	3.1	2754	4	US-09-252-991A-8530	Sequence 8530, Ap
17	99.6	3.1	672	4	US-09-252-991A-14411	Sequence 14411, A
18	99.6	3.1	1530	4	US-09-252-991A-14293	Sequence 14293, A
19	99.6	3.1	3594	4	US-09-252-991A-14262	Sequence 14262, A
20	87.2	2.7	260	3	US-08-735-545-24	Sequence 24, Appl
21	87.2	2.7	260	3	US-09-449-083-24	Sequence 24, Appl
22	87.2	2.5	1443	4	US-09-252-991A-8318	Sequence 8318, Ap
23	74.6	2.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
24	73	2.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
25	70.8	2.2	1515	4	US-09-543-681A-2618	Sequence 2618, Ap
26	68.8	2.1	2111	4	US-10-096-571-11	Sequence 11, Appl
27	68.8	2.1	2111	4	US-10-096-571-13	Sequence 13, Appl
c 28	65.2	2.0	1833	2	US-08-403-852D-6	Sequence 6, Appli
c 29	65.2	2.0	1833	3	US-08-510-646B-6	Sequence 6, Appli
c 30	65.2	2.0	1833	3	US-09-231-818-6	Sequence 6, Appli
c 31	65.2	2.0	1833	3	US-09-635-359B-6	Sequence 6, Appli
32	65.2	2.0	3390	3	US-09-550-338-1	Sequence 1, Appli
33	65.2	2.0	3390	4	US-09-767-878-1	Sequence 1, Appli
34	61.4	1.9	1776	4	US-09-583-110-152	Sequence 152, App
c 35	60.8	1.9	2841	2	US-08-452-075-1	Sequence 1, Appli
36	60.8	1.9	2841	3	US-09-231-061-1	Sequence 1, Appli
37	60.8	1.9	2841	3	US-09-011-762-5	Sequence 5, Appli
38	60.6	1.9	1587	4	US-09-489-039A-2568	Sequence 2568, Ap
c 39	59.8	1.8	25002	4	US-09-489-039A-840	Sequence 840, App
c 40	58	1.8	1689	3	US-09-103-840A-2	Sequence 2, Appli
c 41	58	1.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 42	57	1.7	1830121	4	US-08-961-527-48	Sequence 48, Appl
43	55.8	1.7	1830121	4	US-09-557-884-1	Sequence 1, Appli
44	55.8	1.7	1830121	4	US-09-643-990A-1	Sequence 1, Appli
45	55.8	1.7	1830121	4	US-10-329-960-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-543-681A-4139

; Sequence 4139, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4139
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4139

Query Match   11.3%;   Score 366.2;   DB 4;   Length 1746;
Best Local Similarity   53.7%;
Matches   899;   Conservative   0;   Mismatches   758;   Indels   18;   Gaps   6;

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Qy    849 AGGTGTGAAGCGAATTTATGGTTTGGTTGGGGTGACAGCCTTAATCCGATCGTGCGATGCTGT  908
          ||||||||| |||||| || ||||||||| ||| || ||||| |||||||||||||| ||||
Db     72 AGGTGTGAAACCTTATTTGGGGGGGTGACGGGGCGGATTCATTGAATGGATTAAGTGAATAGCTT  131

Qy    909 CCGCCAATCAGAT--ATTGAGTGTGGGTGCACGTTCGAAAATGAGGAGGAGCGCGGGCGGCGTTTTGC  965
          ||||||||||||   |||||||||| |||||||||||||||||||||||||||||| || ||||| |||
Db    132 GCGCAAAATGGGTACCATTGAATGAGTAGGGCACACGCCATGAAGAAGTCGCGCGGCTTTTGC  191

Qy    966 AGCCGGTGCGGAAATCGTTGATCACTGGGGAGGGCGAGTATGTGCTGCTTCTTGTGGTCC  1025
          |||||||| ||||||||| |||| || || |||||  ||||| || |||||| || || |||
Db    192 CGCCGGAGCAGAAGCGGCTATCAAATGGTGAATTAGCCGTTGTGCCGGCTCCCTGGTGGACC  251

Qy   1026 TGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAAATGCGGCGAAGGTGTT  1085
          |||| || |||| |||||||||||| ||| || || |||||||||||| ||| ||||| |||
Db    252 AGGTAACTTACACTTAATTAATTAATGGACTTTTTGAATTGCATCGTAAATCAAGTTCCCGTGTT  311

Qy   1086 CGGCCATCCGCTAGCCACCATATTCCGAGTGCCCCACGATTGGTTCGACGTTCTTCCAGGAAACGCA  1145
          |||| ||| || ||| |||||||||| |||||| |||||| ||||| ||||| |||||||||||||||
Db    312 AGCGATTGCCCGCTCAATATTCCCTCGCTGCTGAAAATTGGTTAGTAATTACTTTCAAGAAAACTCA  371

Qy   1146 TCCGGAGAGATTTGTTTTAAGGAAATGCTCTGGTTACTGGCGAGATGGTGAATGGTGGTGAGCA  1205
          ||||| ||||||||||| ||||||| ||| || |||||| || ||| ||| |||| |||| |||||
Db    372 TCCTCAAGAGTTATTTCGTGAATGAGTCACTATTGTGAATTAGTCTCTAATCCGATCA  431

Qy   1206 GGGTGAACGCATTTTGCATCACGCGATTCCACCATGGCGGGGTAAAGGTGTGTCGGT  1265
          |||||||| ||| ||| |||||| |||| || ||| || || |||||||||||||
Db   1206 GGGTGAACGCATTTTGCATCACGCGATTCCACCATGGCGGGGTAAAGGTGTGTCGGT  1265
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RESULT 2
US-09-489-039A-4884

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;   Sequence 4884, Application US/0489039A
;   Patent No. 6610836
;   GENERAL INFORMATION:
;     APPLICANT: Gary Breton et. al
;     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;     TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;     FILE REFERENCE: 2709.2004001
;     CURRENT APPLICATION NUMBER: US/09/489,039A
;     CURRENT FILING DATE: 2000-01-27
;     PRIOR APPLICATION NUMBER: US 60/117,747
;     PRIOR FILING DATE: 1999-01-29
;     NUMBER OF SEQ ID NOS: 14342
;   SEQ ID NO 4884
;     LENGTH: 1749
;     TYPE: DNA
;     ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4884

  Query Match             11.2%;  Score 362.8;  DB 4;  Length 1749;
  Best Local Similarity   52.8%;  Pred. No. 2e-103;
  Matches   909;  Conservative    0;  Mismatches  792;  Indels   21;  Gaps  5;
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Qy    802 ATGGCACACAGCTACCGAGAACAAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGGGA 861
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Db     31 ATGAAACAGACCCTGGCCGCGGCATACACATTGCCAAAAACGCTGGAACACAGGCGAACGT 90

Qy    862 ATTTATGGTTTGGTGGGTGACAGCCTTAAT---CCGATCGTGGATGCTGTCGGCCAATCA 918
          | |||||| || | ||||||| || |   |      |   | | ||| | |   ||  |
Db     91 ATCTGAGCCGCGTCACCGGAGATTCCCCTCAAATGGATCAGAGCCTTAACCGCATGGGGC 150

Qy    919 GATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCCGGTTTGCCAGCCCGGCGGA 978
          |||||   | |  || |||| || || || || | | ||| | ||  ||| | || ||
Db    151 ACCATCGACTGGATGCCCACCCGGCACGAGAGGTCGCCGCTTTGCGCTGCGCCGGGGAA 210

Qy    979 TCGTTGGATCACTGGGAGGAGCTGCGGAGTAATGTGCTGCTTCTTGTGGTCCTGGAAACACACAC 1038
          | |  ||| |  ||   || | || || | | | || | ||  | ||  |    ||| ||  ||
Db    211 GGCGAGCTGACCGGCGAGCCTGGGGGCTCGCCGGCCGGGGACCGGGCGAAACCTGCAC 270

Qy   1039 CTGATTCAGGGTCTTTATGATTCGAATCGAAATGGTGCGAAGGTGTTGGGCCATCGCTAGC 1098
          | | | ||||  ||  || ||| || || |  ||  | ||  ||| || |||  || |
Db    271 CTGATTAACGGTTTTGTTGACTGTCATCGGCGAACCATGTCCCGGCGTGGCCATCGCGCC 330

Qy   1099 CATAATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCTCCAGGAAACCCATCGGGAGATTTTG 1158
          |||  || ||| ||||| ||||||  ||  || || || ||| ||  || ||| |||| |
Db    331 CACATCCATCCAGCGAAATCGCGACCGGCTATTTCAGGAAAACCCATCTCAGAGCTG 390

Qy   1159 TTTAAGGAAATGCTTCTGGATTCACTGGTTACTGCGGAGATGGTGAATGGTGGGAACGGCATT 1218
          ||  ||| |  ||| | || ||| || |  || ||||||  || | || | ||| ||||
Db    391 TTCCCGGCAGTGCAGCCATTACTGCGAACTGGTCTCCACCGCGAGCGATCCGGCAGGTG 450

Qy   1219 TTGCATCACGGCGATTCAGTCCAATGGCGGGTAAAGGTGTGTCGGGTAGTGATTCCT 1278
          ||  ||||   | || | || |||  | |||  | | |  | ||   |||   ||  |
Db    451 CTGGCAGTGGCGATGCGTAAGGAGGCAGTGATTAACCGCGGGCTTCTCGGTGGTGTTGCCC 510

Qy   1279 GGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAAATTCCACTATTTCTTCT 1338
          |||  | ||| | ||   || | || || ||  ||    |   ||  ||||  |  |  |
Db    511 GGCGGATGTGGCCTAAGGAAAGCGCCCAGGAGCCACTGGTATCATGGCGC- 569
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Qy    432 GATCCCACAAAATTCTGGCTATCGCCTATGCCGCACCGCTATTTGAAAAAGGGTGTTGCGT 491
          | |   || ||  ||  |||||  |  |  |||| || | ||| ||| |  || |||| |||
Db    491 GGTAGTGATTCCTGCTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTC 550

Qy    492 GGTGGTATTACCCGGTGATGTAGCGGTTAAAACCCGGCTCCAGAAGAATGCCCATGAAAATT- 550
          || || || || |||  | || | ||  ||  |  | || || || || | |  | | |
Db    551 --GGTATCCACTACCAATCACCACTGATTATGCCGGAATCGTTTTGAAATCGAAAACTGTC 608

Qy    551 --GGTATATCCACTACCAATCACCACTGATTATGCCGGAATCGTTTTGAAATCGAAAACTGTC 608
          ...
Db    609 TGAGGCACTGAATAACGCTAAAAAATATCACCTTAAATGTGTGGTGCCGGTTGTGCTCAAGC 668

Qy    609 TGAGGCACTGAATAACGCTAAAAAATATCACCTTAAATGTGTGGTGCCGGTTGTGCTCAAGC 668
Db    669 ACATGATGAGAAGTGGTGAAAACTAGCACAAACCCTGTTCTGTGCATCACTACG 728

Qy    669 ACATGATGAGAAGTGGTGAAAACTAGCACAAACCCTGTTCTGTGCATCACTACG 728
Db    729 TGGGAAAGTATCTTGAGTGGAATAATCCATGTAGCCGTGGGAATAGACGGTTCTTATCGG 788

Qy    729 TGGGAAAGTATCTTGAGTGGAATAATCCATGTAGCCGTGGGAATAGACGGTTCTTATCGG 788
Db    789 TTTTTCATCGGGTTATCACGCAATGGGAGAAATGGGGGATCGTTGCTGATTCTATTGGGA 848

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Qy    849 ATTCCCTTATCGCGCTTTCTATCCTGCCAAAGCTAATATATTATTCAAATTGAACCTTAATCC 908
Db    909 AAGTAGTTATTGGCTCACATTGCCATGTGGATATGGCTTTTGTTGGAGTGTCAAAGCACAAC 968

Qy    909 AAGTAGTTATTGGCTCACATTGCCATGTGGATATGGCTTTTGTTGGAGTGTCAAAGCACAAC 968
Db    969 CCTTAATGCATTACAACCGCGATTAAAAGAGAAAAACAGATACCGGACCATCTTGATGCCTC 1028

Qy    969 CCTTAATGCATTACAACCGCGATTAAAAGAGAAAAACAGATACCGGACCATCTTGATGCCTC 1028
Db   1029 GTTAAA---ACATTAATGCTAAAGCACAGCAAAGATTTAGAGTGATACAACTAGTG- 1084

Qy   1029 GTTAAA---ACATTAATGCTAAAGCACAGCAAAGATTTAGAGTGATACAACTAGTG- 1084
Db   1085 --AGCGTGAGTTGATCCACCCTCAGTTATTTGAAACGACTGGCGGGGATAA 1142

Qy   1085 --AGCGTGAGTTGATCCACCCTCAGTTATTTGAAACGACTGGCGGGGATAA 1142
Db   1143 TGATCGGGTTATTTACCTGTGAAGTTGGCAGCCAACAGTTTGGGCAGCACGTTA---CGT 1199

Qy   1143 TGATCGGGTTATTTACCTGTGAAGTTGGCAGCCAACAGTTTGGGCAGCACGTTA---CGT 1199
Db   1200 GAAAATGAATGGTAAACGTCGTTTAAATTGGTTCATTTAAATGGCGAATGC 1259

Qy   1200 GAAAATGAATGGTAAACGTCGTTTAAATTGGTTCATTTAAATGGCGAATGC 1259
Db   1260 GATGCGCAAGCTCATGCGAAAGTTGATTGGTATTCAAGCACTGACAGAAAACGTCAAGTTGTGTGGCGATGTG 1319

Qy   1260 GATGCGCAAGCTCATGCGAAAGTTGATTGGTATTCAAGCACTGACAGAAAACGTCAAGTTGTGTGGCGATGTG 1319
Db   1320 CGGTTGACGGTGGTTTTAACCATTGGANTCATTCTCATTGGCTCAAATGAACTT 1379

Qy   1320 CGGTTGACGGTGGTTTTAACCATTGGANTCATTCTCATTGGCTCAAATGAACTT 1379
Db   1380 ACCGGTGAAAGTGGTGGATTTTTATAAACAGGTGTTCTTTGGGCATGGTGAAGTTGGAGTATGGGCT 1439

Qy   1380 ACCGGTGAAAGTGGTGGATTTTTATAAACAGGTGTTCTTTGGGCATGGTGAAGTTGGAGTATGGGCT 1439
Db   1440 AGGGGGGGGCTATTTGACTGATGGCACCGATTTACTAATAATCCTGATTTGCCGGTAATTGC 1499

Qy   1440 AGGGGGGGGCTATTTGACTGATGGCACCGATTTACTAATAATCCTGATTTGCCGGTAATTGC 1499
Db   1500 CAATGCCGCGGGGAATTTAAAAGGTATTCCGCTTGAGAAGAAAGAGATCTTGANTGAAGCATT 1559

Qy   1500 CAATGCCGCGGGGAATTTAAAAGGTATTCCGCTTGAGAAGAAAGAGATCTTGANTGAAGCATT 1559
Db   1560 AAAAACAGCCCTTTGAACATGAGGCCCCTGTTATTGTGGAATGTGGTAACCCGGAAAACAGAA 1619

Qy   1560 AAAAACAGCCCTTTGAACATGAGGCCCCTGTTATTGTGGAATGTGGTAACCCGGAAAACAGAA 1619
Db   1620 GCTTTCCATTGCCTCCGAAAATTAAAATTGAGCAGCGCAAAGGTTTGATGGCCCAC 1679

Qy   1620 GCTTTCCATTGCCTCCGAAAATTAAAATTGAGCAGCGCAAAGGTTTGATGGCCCAC 1679
Db   1680 GAAAGCGATTATTAATGGTCGTTGGGCGATGAAATTAGTGCAATTAGCGAAAAACCAAC 1734

Qy   1680 GAAAGCGATTATTAATGGTCGTTGGGCGATGAAATTAGTGCAATTAGCGAAAAACCAAC 1734
Db   1626 TTTCCCTTATTCTGATTTCCTTCCT---AAAGACAACGTTGCCCAGGTGGATATCAACACG 1682

Qy   1626 TTTCCCTTATTCTGATTTCCTTCCT---AAAGACAACGTTGCCCAGGTGGATATCAACACG 1682
Db   1683 TCCGCACATTGGTCGACGTAGCACGGTGAGTATCCGGGTGATCGTTGCTGCTGCAAC 1742

Qy   1683 TCCGCACATTGGTCGACGTAGCACGGTGAGTATCCGGGTGATCGTTGCTGCTGCAAC 1742
Db   1743 AATCGAAAAATATTTTGCCTCATGTGAGGGAAAAACAGATCGTTCCTTCCTTGATCGGAT 1802

Qy   1743 AATCGAAAAATATTTTGCCTCATGTGAGGGAAAAACAGATCGTTCCTTCCTTGATCGGAT 1802
Db   1803 GCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTACACACATACGTCGA 1862

Qy   1803 GCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTACACACATACGTCGA 1862
Db   1863 GAAGCAATGTGCCTATTCACCCTGAATACGTTGCCTCCTATTTTGAAACGACTGGCGGGGATAA 1922

Qy   1863 GAAGCAATGTGCCTATTCACCCTGAATACGTTGCCTCCTATTTTGAAACGACTGGCGGGGATAA 1922
Db   1923 GGATCGGGTGTTTACTGGATAACCGGGCATGTGCAAGTGTTACATCGA 1982

Qy   1923 GGATCGGGTGTTTACTGGATAACCGGGCATGTGCAAGTGTTACATCGA 1982
Db   1983 GAATCCGGAGGGAACGCGCGCCGACTTTGTGGGTTCATTCGCCAGCCATGGCTAATGC 2042

Qy   1983 GAATCCGGAGGGAACGCGCGCCGACTTTGTGGGTTCATTCGCCAGCCATGGCTAATGC 2042
Db   2043 GTTGCCCTCATGCGATTGGTGTCCGCGAAAGTTGATCGATCGATGTG 2102

Qy   2043 GTTGCCCTCATGCGATTGGTGTCCGCGAAAGTTGATCGATCGATGTG 2102
Db   2103 TGGGCCATGGTGTTTGGGCCATGAGTGTCGACCGTTAAGCTTGCACCGAATGG 2162

Qy   2103 TGGGCCATGGTGTTTGGGCCATGAGTGTCGACCGTTAAGCTTGCACCGAATGG 2162
Db   2163 TCCGCTGAAGGCTGGTGTGTTAACACAGTTCTTTGGGCATGGTGAAAGTTGGAGATGGCT 2222

Qy   2163 TCCGCTGAAGGCTGGTGTGTTAACACAGTTCTTTGGGCATGGTGAAAGTTGGAGATGGCT 2222
Db   2223 CGTGGAGGGACAGCCAGAATTTGGGTACTGACAAGTGAAATTCGGCGAAGCGGCGCCAC 2282

Qy   2223 CGTGGAGGGACAGCCAGAATTTGGGTACTGACAAGTGAAATTCGGCGAAGCGGCGCCAC 2282
Db   2283 GGCGGCTTGCGGTTATCAAATCGGTAGCGGATCACCGATCCGGAAGAGAGATCTTGANTGAAGCATT 2342

Qy   2283 GGCGGCTTGCGGTTATCAAATCGGTAGCGGATCACCGATCCGGAAGAGAGATCTTGANTGAAGCATT 2342
Db   2343 AGCTGAGGCATTGGCATAATCCTGGGACCTTGATCGATATAGTCACGGATCCTAAGTGC 2402

Qy   2343 AGCTGAGGCATTGGCATAATCCTGGGACCTTGATCGATATAGTCACGGATCCTAAGTGC 2402
Db   2403 GCTGTCGATCCCACCGAACCATCACGTGGGGACACAGGTCATGGAACAAAGGCGGCCAC 2462

Qy   2403 GCTGTCGATCCCACCGAACCATCACGTGGGGACACAGGTCATGGAACAAAGGCGGCCAC 2462
Db   2463 CCGAACCGTCTTGGTGGAGGAGGTAGGAGCGGATGATCGATCTGGACGGGCCGTTCGAAC 2517
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RESULT 3
US-10-096-571-1
; Sequence 1, Application US/10096571
; Patent No. 6623944
; GENERAL INFORMATION:
;   APPLICANT: RIEPING, MECHTHILD
;   TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the
;   FILE REFERENCE: 211499
;   CURRENT APPLICATION NUMBER: US/10/096,571
;   CURRENT FILING DATE: 2002-03-14
;   PRIOR APPLICATION NUMBER: DE 10112102.4
;   PRIOR FILING DATE: 2001-03-14
;   PRIOR APPLICATION NUMBER: US 60/304,776
;   PRIOR FILING DATE: 2001-07-13
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
;   LENGTH: 1719
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1716)
;   OTHER INFORMATION:
US-10-096-571-1

Query Match   9.4%; Score 305.2; DB 4; Length 1719;
Best Local Similarity   50.7%; Pred. No. 2.8e-85;
Matches 873; Conservative 0; Mismatches 828; Indels 21; Gaps 5;

Qy   802 ATGGCACAGCTACCGCCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAAACAAACGGTTCGCTTGCAGCTTAATCGCCAAAAACACTGAATCGGCAGGGTGAAACGC 60

Qy   862 ATTTATGCGTTTGGGTGGGTGCTGCAGACGCCTTAA---TCCGATCGTGGATGCTGCCAATCA 918
          ||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   61 ATCTCGGGAGTCACAGGCGACTCTCTTGAACACGGTCTTAGTGACAGTCATGGGC 120

Qy   919 GATATTGAGTGGGTGCACGTTGCGAAATGAGGAAAAGCGCGGCGGGGTTGCGGGA 978
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACCATCGAGTGGAATGTCCACCCGCCACGAAGAAGTGGGGCGCCTTTGCCGTGCCGAA 180

Qy   979 TCGTTGATCACTCGGGGAGAGCTCGCAGTATGTCGCTGCTTCTTCGTTGTGGAAACACACAC 1038
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCACAACTTACGGAGAACTGGCGCGGTCGCGCCGGATCGGTGGCCATCGCGTAGC 240

Qy   1039 CTGATTCAGGGGTTCTTTATTGATTCGCATCGAAATGGTGCGAAGGGTGTTGGCCATCGCTAGC 1098
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTAATCAAACGGCCGTTGTCGAATGCCACCGCAATCACGTTCCGGTTACTGGCCGGATTGCGCT 300

Qy   1099 CATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGGCATCCCGAGATTTTG 1158
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CATATTCCCTCCAGCGAAATTGGCAGCGGCGCTGTTTTCCAGGAAAACCCACCACAAGAGCTA 360

Qy   1159 TTTAAGGAAATGCTCTCGGTTACTGCCGAGATAGTTGAATGGGTTGGAGACCGCATT 1218
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TTCCGGCGAATGTTAGTGCTACTATTGCCGAGTCAGCCGGTGCCTGGGGTAAAGGTGTGAACGGTA 420

Qy   1219 TTGCATCACGCGGATTCAGTCCACCATGAGCGGGGTAAAGGTGTTGGGTAGTGATTCCT 1278
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGGGCGGATTCGCATCGGCAAAGCGTGCTTAACCGGTGCTACTCTTTATTCCACTATTTCTCT 480

RESULT 4
US-09-252-991A-7335
; Sequence 7335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7335
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7335

```
               || |   |        || | |   |    |   ||  |   | |||  |||    ||
Db         582 CCAGCGACGCCGAACTGCAGGACGTCGCCCGCCTGC--TGGCCCACGGCAAGAAGATCGG 639

Qy        1416 TTTGTTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAA 1475
                 | | |  |||  | |||    ||   || | ||  | | || |||   | || ||
Db         640 CATCTACGCCGGCTCCGGCTGCCAGGGCGCCCACGACCTGCTGGTGGCCCTCGCCGACCG 699

Qy        1476 GATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCC 1535
                 | ||  | || |||| |||  ||  | | |  ||| | | | || || | || || ||
Db         700 CCTCAAGGCGCCCATCGCGCACACGTCGCGGGCCAAGGACTTCGTCGAGTACGACAACCC 759

Qy        1536 GTTTGAGGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGA 1595
                ||  |  | |||||| | ||  |||| ||   ||   || || |  |   |   |  ||
Db         760 CTTCAACATGGGCATGACCGGTATGCTCGGGATCGAGTCCGGCTTCCACATGATGACCGA 819

Qy        1596 GGCGGATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCC---TAA 1652
               |   ||    ||  | ||  | ||  | || ||| | |   |  | |||  |||    ||
Db         820 GTGCGACACCCTCCTGCTGCTCGGCGCCGACTTCGCCTGGGCGCAGTTCTATCCGCAGAA 879

Qy        1653 AGACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAA 1712
                | || | |   |||||| ||   | | ||    ||| | || || ||   | |  |  |
Db         880 GGCCACCCTGATCCAGGTCGACCGCGATGGCAGTCACCTGGGCCGCCGCCACCCCATCGA 939

Qy        1713 GTATCCGGTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGA 1772
                      |||  ||| || ||     |           |  | |||||     |  | |
Db         940 TCTCGGCGTGGTCGGCGACGTGATCCC----------CAGCTCTTGCCGTTGCTCGAAGC 989

Qy        1773 AAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTC 1832
                      || ||   ||||| | ||       ||  ||   | ||||||   | || |  |
Db         990 CCGCGAGGAGCGCAGCTTCCTCGACGAATGCCTGGAGCACCGCGAGCGCTCGCTGCGGAC 1049

Qy        1833 GGTGGTAGAGACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGT 1892
               | ||| | |   | |   |      | ||  |||   | ||  || || ||  |  || |
Db        1050 GCTGGAAAAAGAGGAGCAA------GCCGGCAAGGGCGAGCTGATCCATCCGCAGCACCT 1103

Qy        1893 TGCCTCTATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCAT 1952
                | |    |  |  || |||  ||     |||| ||  |||| || |  ||   ||||
Db        1104 GGTCAGCCTGCTCGACCAGCACGCCAGCGAGGACGCCCTGTTCACCGCCGACGGCGGCTC 1163

Qy        1953 GTGCAATGTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGG 2012
               |   |  || ||||    | |  ||||| | |      | || | ||||  |    |
Db        1164 GGCGATGGTCTGGCTGTTGCGTCACATCCACA---GCAACGGCAAGCGCCGCACCCTCAC 1220

Qy        2013 TTCATTCCGCCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGT 2072
                    |   ||||||||| ||||| || ||  |||| || ||| | ||   | | |  |
Db        1221 CAGCCTGGTCCACGGCACCATGGCCAACGCCATGCCCCAGGCGCTGGGGCTGAAGAAGGC 1280

Qy        2073 TGATCGAAACCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGG 2132
                 | |   | |||||||||||| |||| |  ||||| || ||  ||| ||||||||| ||
Db        1281 CTACCCCGAGCGCCAGGTGATCTCGATCTCCGGCGACGGCGGCCTGGCCATGCTGCTCGG 1340

Qy        2133 TGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAG 2192
                || || ||||| |  |   | |  |||| ||| | ||||  |||||| | |||||
Db        1341 CGACCTGCTGACGGCCATCCAGGAAAAACTGCCGATCAAGGTAGTGGTGCTGAACAATGC 1400

Qy        2193 TTCTTTGGGCATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGA 2252
                ||  ||  | | ||  || ||||   |   || ||||| | ||  ||       || ||
Db        1401 CTCGCTGAACTTCGTCGAGCTGGAACAGAAGGTCGAGGGCCTGCTGGACAGCTACACCGA 1460

Qy        2253 CCATGAGGAAGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCAT 2312
               ||      |   | | |||||     | || |  |     ||  || |           |
Db        1461 CCTGCTCAACCCGGACTTCGCCCGTCTCGCCGAAGTGATCGGCTTCCACGGACGCAAGGT 1520

Qy        2313 CACCGATCCGAAGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGT 2372
                ||     |  || |  |      |  | |    |||    | ||  | || || || |
Db        1521 GACGCGCTCCGAGGAGCTCGAGACGGCGGTGCAGGAGTTCCTCGCCCAGCCCGGTCCGGC 1580

Qy        2373 ACTGATCGATATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACCATCACGTGGGA 2432
                ||| | ||  |    ||  | |||   | ||||  ||| || || |  |||  ||  |
Db        1581 GCTGCTGGACGTGCATACCAACCCTGCGGAGCTGGTGATGCCGCCGAAGATCGAGTTCGG 1640

Qy        2433 ACAGGTC 2439
                ||||||
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Db        1641 CCAGGTC 1647

RESULT 5
US-09-489-039A-4905/c
; Sequence 4905, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 4905
;   LENGTH: 1293
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4905

  Query Match              7.0%;  Score 227.4;  DB 4;  Length 1293;
  Best Local Similarity   52.0%;  Pred. No. 7.6e-61;
  Matches  641;  Conservative    0;  Mismatches  571;  Indels   21;  Gaps    5;

Qy         802 ATGGCACACAGCTACGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 861
               |||  ||| | |   || | | |  |     | ||  ||||||      || ||||| ||
Db        1218 ATGAAACAGACCGTGGCGGCATACATTGCCAAAACGCTGGAACAGGCCGGCGTGAAACGT 1159

Qy         862 ATTTATGGTTTGGTGGGTGACAGCCTTAAT---CCGATCGTGGATGCTGTCCGCCAATCA 918
               || |  ||  |    || ||   ||| |||     || ||       |  ||||
Db        1158 ATCTGGGGCGTCACCGGAGATTCCCTCAATGGATTGAGCGATAGCCTTAACCGCATGGGC 1099

Qy         919 GATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAA 978
                  || || ||| ||| |   ||  | || || |  || || || || || || ||||||
Db        1098 ACCATCGACTGGATGCCCACCCGGCACGAAGAGGTCGCCGCTTTCGCCGCTGGCGCGGAA 1039

Qy         979 TCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACAC 1038
                ||  | | || || |||||||| || || || |  || || || || || |||   |||
Db        1038 GCGCAGCTGACCGGCGAGCTGGCGGTCTGCGCCGGCTCCTGCGGACCGGGCAACCTGCAC 979

Qy        1039 CTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGC 1098
               |||||| | ||| | | ||| |  ||||| ||   ||    |||| ||||||||||   |
Db         978 CTGATTAACGGTTTGTTTGACTGTCATCGCAACCATGTCCCGGTGCTGGCCATCGCCGCC 919

Qy        1099 CATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTG 1158
               || || ||      | | || ||       |  || ||||||||| |||||  ||    ||
Db         918 CACATCCCATCCAGCGAAATCGGCAGCGGCTATTTTCAGGAAACCCATCCTCAGGAGCTG 859

Qy        1159 TTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATT 1218
               ||    || |||     |||||||||  ||||          ||||||      |   |
Db         858 TTCCGCGAGTGCAGCCATTACTGCGAACTGGTCTCCACGCCGGAGCAGATCCCGCAGGTG 799

Qy        1219 TTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCT 1278
                ||      ||||| |      |  ||         || || ||||||||| ||| | ||
Db         798 CTGGCAGTGGCGATGCGTAAGGCAGTGATTAACCGCGGCGTCTCGGTGGTGGTGTTGCCC 739

Qy        1279 GGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCT 1338
               || ||| | ||   | | | |||    ||  |  |      | | |    |  | |  |
Db         738 GGCGATGTGGCGCTGAAGGCCGCCCCGGAAAGCGCCAGCAGCCACTGGTATCATGCGCCG 679

Qy        1339 GGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAAC 1398
                   |  |   |||   |||||        |||        ||||| | ||   |||  |
Db         678 CTGCCGAC---GGTCACCCCGGCGGAAGAAGAGCTGCGCAAGCTGGCGCAGCTTATTCGC 622

Qy        1399 AACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTG 1458
                || | |    | || |  |  | |||||    ||          || | |  | |  ||
Db         621 TACTCCAGCAATATCGCGCTCATGTGCGGCAGCGGTTGCGCCGGCGCCCACCAGGAACTG 562

Qy        1459 TTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTAC 1518
                ||||||| || |  || |||||| | || ||||  || || ||| | || ||  || ||
```

RESULT 6
US-09-252-991A-7413
Sequence 7413, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7413
LENGTH: 1083
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa

Query Match   50.9%;
Best Local Similarity   50.9%;
Matches   469; Conservative   0; Mismatches 443; Indels   9; Gaps   3;
Score 164.2; DB 4; Length 1083;
5.1%; Pred. No. 5.5e-41;

```
Qy     33 AAACGCGCCCTGCTGGGCTTCGTTCAACCACGGC 1
                                              1
Db   2028 ACCGCGCGACTTTGTGGGTTCATTCCGCCACGGC 1996

Qy   1996 ACCGCGCGACTTTGTGGGTTCATTCCGCCACGGC
Db     90 ACCTGTGATGTCGGGCACCCCGACCGTCTGGGGG  ... 34

Qy     90 ACCTGTGATGTCGGGCACCCCGACCGTCTGGGGG
Db   1936 ACTGTGGATACCGGCGCATGTGCCAATGTTGTGG  ... 1995
```
(alignment continues)

RESULT 7
US-09-252-991A-7281/c
Sequence 7281, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7281
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7281

Query Match   5.1%;   Score 164.2; DB 4; Length 1113;
Best Local Similarity   50.9%; Pred. No. 5.6e-41;
Matches 469; Conservative 0; Mismatches 443; Indels 9; Gaps 3;

```
Qy   816 CGCAGAACAATTAATTGACACTTTGAAGCTGATGAAGGTGTGAAGGCGAATTTATGGTTTGGT 875
             |||| ||   |||||     |   |||||  ||| |  |  ||| |||||| ||  ||||||
Db  1060 CGCCCGAGATCGTCGTGGAAAACCCTGGAAAGCCGGCGCGTCCCGACCATTGCTAXGGCATCGT 1001

Qy   876 GGGGTGACAGCCTTAATCCGATCGTGGGATGCTGTCTCCGCCAATCAGATTAXTTGAGTGGTGCA 935
             |||| | |||  |||  || | ||||| | |  |  |||||||  || || |  |||||||| 
Db  1000 CGGCGACACCCTCACCATGTCACCGGACCCAGCTCCAGATCCAGTCGTGGGTCCA 941

Qy   936 CGTTCGAAATGAGGAAGGAAGCCGGGGGGCGGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGA 995
             || ||   ||   | || |  |||||| ||||| ||||||| |  ||||||| | |||| ||||
Db   940 CGTGCGCCACGAAGAAGGGGCCTTTGCGCCCGGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGACG 881

Qy   936 TGATTCGCATCGAAATGGTGCGGAAGGTTGGCCATCGTAGCCATTATTCCGAGTGCCCA 995
             ||| |||||     ||||  ||| ||||   |   |||||| | ||||| |||| ||||
Db   940 CGAGGGCCCACGCGCAGGTCGCTGAGTGGCGCCAGTGTCCCTTCGCCGGGGAAATCGTTGATCACTGGGGA 881

Qy  1056 TGATTCGCATCGAAATGGTGCGGAAGGTTGGCCATCGTAGCCATTATTCCGAGTGCCCA 1115
             ||| |||||     ||||  ||| ||||   |   |||||| | ||||| |||| ||||
Db   820 CGAGCGCCCACGCGCAGGTCGCTGAGTGGCGCCAGTGTCCCTTCGCCGGGGAAATCGTTGATCACTGGGGA 881

Qy   996 GCTGGCCAGTATGTGCTTGCTTCTTGTGGTCCTCGGAAACACACCTGATTCAGGGTCTTTA 1055
             || ||||| | |  |||| ||  |||| ||| |||||||| ||| ||||| | |||| || 
Db   880 CCTGACCGCCTGCGCCCGGCTCCTGCGGACACCGGCAGCCCACGTGGGTCCA 821

Qy  1116 GATTGGTTCGACGTTCTTCTTCAGGAAAACGCATCCGGAGATTTTGTTTAAGGAAATGCTCTGG 1175
             |||||| ||| |||||| |||||||   ||| | || ||||||||||| |||||  | |||||
Db   760 ACTGGGCCATGGAGTTTCCCCAGGAGTCGACTTCAGAGGCGGGTCAGGCGTGGGTCCTTA 701

Qy  1176 TTACTGCGAGATGCGGTGAATGGTCGGTCAGCAGGGTGAACGCATTTTGCATCACGCGGATTCA 1235
             |||| | |||   |  ||||  | ||  | |||||| | | |  ||||| |||| |||| ||||
Db   700 GTTCTCGGAGCAGGTGCACACCCGGAACACGGCCGGGTGGGTGGCCTTGCCA 641

Qy  1236 GTCCACCATGGCGGGGGTAAAGGTGTGTCGGTTGGTGGTGAGTTCATCGCTAAGGA 1295
             ||| ||||| | |  |||   | |  ||  |||  ||||| | ||| | || |||||
Db   640 GGCGCGCTCAACCGCGCGGTTGCGGTGTTGATCCTGCGGCGACATC----AGCC 585

Qy  1296 AGACCGAGGTGACGGTGACTTATTCCAATTCCACTATTTCTTCGGCACTCCTGTGGTGTT 1355
             ||| ||||  |  | | |||  |||| ||||| |  || ||| | |  || ||||| |||
Db   584 AGGCCACGGTGAAGGACGACCTGCGTTCTCGGGTGCATTCGGCAACCGGGTGCTGCGGGCC 525

Qy  1356 CCCGGATCCTTACTGAGGCTGCAGAGGGGGATTAACACGGCTAAGTCTGTCAC 1415
             |||| |||  | || |   | | |||  | ||| |||  | ||| |  | |||
Db   524 CCAGCCACGCGCCGAACTGCAGAGGCGTCGCCCCCTGC---TTGCCCACGGCGAAGAGAGCGG 467

Qy  1416 TTTGTTCTGCCGGTGCGGGCGGGGGTGAGAGAATGCTCGGCGGCCCCAGGGTGTTGGAGTTGGCGGAGAA 1475
             ||| || | |   || |||  |||| || ||| | || |||||||||||  | |||||| |||||| | 
Db   466 CATCTAGCGCGCGGCTCGGGCTGCCCACACAGCTTGGGGTGGGCCCTTGCCGGGACCG 407

Qy  1476 GATTAAATCACCGATCGGGGCATGCGCCGTCGGGGTGGTAAGCAGTACATCCAGCATGAGAATCC 1535
             || |  |||| |  || ||| | | ||| |  ||| |||  |||||| | |||| ||| ||||||
Db   406 CCTCAAGGCGGCCCATCGGCACAGGCGTCAGCACC 347

Qy  1536 GTTTGAGGTCGGCCAATGTCTCGGCCTTGGTTACGGTGGATGCGGTCTCCAATGA 1595
             || |||||| |||| |  | ||||| |||||  ||| || ||| |||| | ||||
Db   346 CTTCAAACATGGGCATGACCGGTATCGGCCGTAGTGCCGTCCAATGA 287

Qy  1536 CTTCAAACATGGGCATGACCGGTATCGGCCGTAGTGCCGTCCAATGA 1595
             || |||||| |||| |  | ||||| ||| ||| || ||| |  | 
Db  1596 GGCGGGATCTCGTGATTCTATTGGGGTACGGAGTTTCTTTTCCTTCCT----AA 1652

Qy  1596 GGCGGGATCTCGTGATTCTATTGGGGTACGGAGTTTCTTTTCCTTCCT----AA 1652
             || |   || | || |||| ||||| |||| ||| |  |||| |||||    || 
Db   286 GTGCGCACCCTCCTGCTGGCCCGACTTCGGCCGCAGTTCTATCCGCAGAA 227

Qy  1653 AGACAACGTTGCCCAGGTGAATATCAACGTGCGCAGTACGACCGGTGAA 1712
             ||| | |||||||| |||| | | || |||||| ||| ||| ||||| 
Db   226 GGCCACCCTGATTCAGGTCGACGCGATGGCAGTCACCTGGGCCGCGCCACCCCATTCGA 167

Qy  1653 GGCCACCCTGATTCAGGTCGACGCGATGGCAGTCACCTGGGCCGCGCCACCCCATTCGA 1712
             ||| |||||| || ||| | | |||| ||| |||| ||| || |  |||||  ||  | 
Db  1713 GTATCGGGTTGACCGGTGATGT 1733

Qy  1713 GTATCGGGTTGACCGGTGATGT 1733
               ||||| |||| | ||||| | 
Db   166 TCTCGGGTCGGTCGGCGACGT 146
```

RESULT 8
US-10-096-571-7
; Sequence 7, Application US/10096571
; Patent No. 6623944

; SEQ ID NO 7
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1454)
; OTHER INFORMATION: Mutagene DNA
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (57)..(577)
; OTHER INFORMATION: Part of the 5' region (poxB1) of the poxB gene
; NAME/KEY: misc_feature
; LOCATION: (578)..(646)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (647)..(1398)
; OTHER INFORMATION: Part of the 3' region (poxB2) of the poxB gene
; NAME/KEY: misc_feature
; LOCATION: (1399)..(1454)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
US-10-096-571-7

Query Match   4.8%;   Score 155; DB 4; Length 1454;
Best Local Similarity   53.7%; Pred. No. 5.3e-38;
Matches 345; Conservative 0; Mismatches 295; Indels 3; Gaps 1;

```
Qy  1874 CTATTCACCCTGAATACGTTGCCTCTATTTGAAACGAGCTGGCGGGATAAGGATGCGGTGT 1933
             ||||||| |||  | || |||| ||| |  |||  | |  ||| || | ||  |  |||| 
Db   768 CCATTCACCCGCCAATANCCTGGCTGCGCGCGCAGCAAATTAGTCATTTTGCGCCGGATGACGCGTATTT 827

Qy  1934 TTACTGTGGATACCGGCGCATGTGCAATGTGTGCATGGCATCGTGAGGATTACATCGGAAGGATCCGGAGG 1993
             |||| ||||| |||||||||||||| ||||| ||||| | ||  || |||   |  | | ||||||| || 
Db   768 TCACCTCTGACCTTGGTACGCCAACGGTGTGGGGCCCACGGTTGTCTACGT---TGAACG 884

Qy  1994 GAACGCGCGACTTGTGGGTTCATTCCGCCACGGCACGGATAGCCTAATGCGTTGCCTCATG 2053
             |||| | |  |||| |||  | || ||||| ||| | || | | |||   |||| | |||| 
Db   828 TCACCTCTGACCTTGGTACGCCAACGGTGTGGGGCCCACGGTTGTCTACGT---TGAACG 884

Qy  2054 CGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCCGCGATGTGTGGCGGATGGTG 2113
             || ||| | ||| |||| ||||| || | |||| |||| |  || ||  | ||| |||| | 
Db   884 GCAAGCGTCGCCCTGTTAGGTTCGGTTCAGTATCCGAATGCCTGATGTGTGGCGGATGGTG 944

Qy  2054 GCAAGCGTCGCCCTGTTAGGTTCGGTTCAGTATCCGAATGCCTGATGTGTGGCGGATGGTG 2113
             || || | | ||  ||| |||| | || || | |||| | || |||| | |||||||| | 
Db  2114 GTTTGGGCCATGCTGCTGGGTGAGCTTCTGACCGGTTAAGCTGCGCACCAACTTCGGTGAAGG 2173

Qy  2114 GTTTGGGCCATGCTGCTGGGTGAGCTTCTGACCGGTTAAGCTGCGCACCAACTTCGGTGAAGG 2173
             || | |||||||| | | ||| |||||||| |||| |||||| |||| ||| || |||| | 
Db  1005 GTTTTTAGCATGTTGATGGGCGATTTCCTCTCAGTAGTGACAGATGAAAACTGACAGTGAAA 1064

Qy  2174 CTGTGGTGTTTTAAACAACACAGTTCTTTGGGCATGGTGAAGTTGGAGATGGATCCTCGTCGGAGGGAC 2233
             || | | ||| |||||| || ||  || |||| ||||| || |  | |||||  || | || ||||| 
Db  1005 TTGTCTGTCTTTAACAACACAGCTGCTCGGGCTTTGTCGCCGGATGGAAAAGCTGTGGTGGCT 1124

Qy  2234 AGCCAGAATTTGTACTGACCATGAGGAAGTGAATTTCGCAGAGATTGCGGCGGGGCTGCG 2293
             |||| | ||| | |  ||||| || ||||| |||| ||||||| ||| ||||||| ||| 
Db  1065 TTGTCGTCTCTTTAACACACAGCTGCTCGGGCTTTGTCGCCGGATGGAAAAGCTGTGGTGGCT 1124
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Db  1125 ATTTGACTACGCGGCACCGAACTACGACGACACAAACTTTGCCCGGCCATTGCCGAAGCCGTGCG 1184
Qy  2294 GTATCAAATCGGTACGCATCACCGATCCGAGCAGCTAGCTGAGGCAT 2353
Db  1185 GCAATTACGGGTATCCGTGTAGAGAAAAAGCGTTCGAAAGTTGATGAAGCCCTCGAACGCGCCT 1244
Qy  2354 TGGCATATCCTGGACCTGTTACTGATCGATCACGGGATCCTAATGCGGTCGTCGGATCC 2413
Db  1245 TCTCCATCGACGGTCCGGTTGTTCGCGGATGTGGTGCGATTC 1304
Qy  2414 CACCAACCATCACGTGGGAACAGGTCATCGGGATTCAGCAAGGCGCCACCCGAACCGTCT 2473
Db  1305 CACCGCAGATCAAACTCGGAACAGGCCAAAAGGTTTCAGCCTGTATATGCTGGCGCAATCA 1364
Qy  2474 TTGGTGGAGGAGTAGGACGGATGAATCGATCCGGCCCCGTTCGAA 2516
Db  1365 TCAGCGGACGCGGGTGATGAAGTGATCGAACTGGCAAGGCGGAA 1407
```

RESULT 9
US-10-096-571-8
Sequence 8, Application US/10096571
Patent No. 6623944
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts th
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8
; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Start codon of the delta poxB allele
; NAME/KEY: misc_feature
; LOCATION: (1)..(605)
; OTHER INFORMATION: 5' region of the delta poxB allele
; NAME/KEY: misc_feature
; LOCATION: (606)..(674)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (675)..(1445)
; OTHER INFORMATION: 3' region of the delta poxB allele
; NAME/KEY: misc_feature
; LOCATION: (1446)..(1448)
; OTHER INFORMATION: Stop codon of the delta poxB allele

US-10-096-571-8

Query Match   4.7%; Score 152.8; DB 4; Length 1448;
Best Local Similarity 53.4%; Pred. No. 2.6e-37;
Matches 344; Conservative 0; Mismatches 297; Indels 3; Gaps 1;

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Qy  1874 CTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGACTGCTGGCCGGCGGATAAGGATGCGGGTGT 1933
Db   796 CCAATCACCCGCAAATATCTGGCCGCCAGCAAATTAGTCATTTGCCGCCGATGACGGCTTATTT 855
Qy  1934 TTACTGTGGATACCGGCATGCTGTGCAAATGTGTGGCGAGGTTACATCGAGAATCCGGAGG 1993
Db   856 TCACCGTGACGTTGGTAGCGCACAACGGTGTGGCGGCGACGTTATCTAAAAA---TGAACG 912
Qy  1994 GAACGCGCGGACTTTGTGGGTTCATTCCGCCACGGACGATGGCTGGTTCATTGCGTTGCCTCCATG 2053
Db   913 GCAAGCCTCGCCTGTTAGGTTCGTTTAACCACGGTTCGATGGCTACCGCCATGCCGCACGG 972
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RESULT 10
US-08-956-171E-138
Sequence 138, Application US/08956171E
Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224

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Qy  2054 CGATTGGTGCGCAAAGTGTTGATCGGAAACCGCCAGTGTGATCGGGATGGTG 2113
Db   973 CGCTGGGTGCGGCAGGGCGACAGAGCCAGAGAACGTCAGGTGGTGCCCAATGTGCGGCGATGGCG 1032
Qy  2114 GTTTGGGGCATGCGTCGGCTGGGTGAGCTTCTGACCGGTTAAGCTGCACCAACTTCCGTGAAGG 2173
Db  1033 GTTTTAGCATGTTGATGGGCGATTCCTCTCAGTAGTGCAGATGAAAACTGCCAGTGAAAA 1092
Qy  2174 CTGTGGGTGTTTAAACACAGTTCTTTGGGCATGGTGAAGTTGGAGATGCTCGTTGGAGGGGAC 2233
Db  1093 TTGTCGTCTTTAACAACAGCGGTGCTGGGCTTTGTGCGGATGGAGATGAGAAAGCTGGTGGCT 1152
Qy  2234 AGCCAGAATTTGGTTACTGACCATGAGGAGGAGTGAATTTCGCGAGAGATTGCGGGCTGCGG 2293
Db  1153 ATTTGACTGACGGCACCGAACTACACGACACAAACTTTGCCCGGCCATTGCCGGAGCCGTGCG 1212
Qy  2294 GTATCAAATCGGTACGCATCACCGATCCGAGAGAAAAAGTTCGCGAGCAGCTAGCTGAGGCAT 2353
Db  1213 GCAATTACGGGTATCCGTGTAGAGAAAAAGCGTTCGAAAGTTGATGAAGCCCTGCAACGCGCCT 1272
Qy  2354 TGGCATATCCTGGACCTGTTACTGATCGATCACGGGATCCTAATGCGGTCGTCGGATCC 2413
Db  1273 TCTCCATCGACGGTCCGGTTGTTCGCGGATGTGGTGCGATTC 1332
Qy  2414 CACCAACCATCACGTGGGAACAGGTCATCGGGATTCAGCAAGGCGCCACCCGAACCGTCT 2473
Db  1333 CACCGCAGATCAAACTCGGAACAGGCCAAAAGGTTTCAGCCTGTATATGCTGGCGCAATCA 1392
Qy  2474 TTGGTGGAGGAGTAGGACGGATGAATCGATCCGGCCCCGTTCGAA 2517
Db  1393 TCAGCGGACGCGGGTGATGAAGTGATCGAACTGGCGAGAAACAAAC 1436
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; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 138:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 7900 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 138:
;
US-08-956-171B-138

Query Match   4.3%; Score 138.8; DB 4; Length 7900;
Best Local Similarity   45.0%; Pred. No. 2.1e-32;
Matches   741; Conservative 0; Mismatches 887; Indels 20; Gaps 5;

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Qy    820 GAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTGTTGGTTGGTCGGT  879
Db   1589 GAAGCATTAGTTAAAGCATTACAAGCATGGGATATAGATCACTTGTATGTATTCCAGGA 1648

Qy    880 GACAGCCTTAATCCGATCGGTGGATGCTGTCCCAATCAGATA-----TTGAGTGGGTGC  934
Db   1649 GACTCAAATCGACACGCATAGTCGATAGTTTACGTGACAGTGAGAGATCAATTTAAATTTTATC 1708

Qy    935 ACGTTCGAAATGAGGAAGCGCGCGGGGCTTTGCAGCCCGGTGCCGGAATCGTTGATCACTGGGG  994
Db   1709 ATGTACGTCATGAAGAAGTACCAAGCTTAGCGGGCTCGTTACACAAAAATTAACTGGTA 1768

Qy    995 AGCTGGCAGTATGTGCTGCTTCTTGTTGGTCTTGGGAAACACACCTGATTCAGGGTCTTT 1054
Db   1769 AAATCGGTGTGCATTAAGTATCGGTTGGCCCTGGTTAATTCATTTATTAAATGTATGT 1828

Qy   1055 ATGATTCGCATCGAAAATGGGTCGGAAGGTGTTGGCCATCGGTCCCC 1114
Db   1829 ATGATGCCAAAATGGATAAAATGTACCGCCAATTAATATATCTCGGACAGAGAATAGTACAG 1888

Qy   1115 AGAATTCGGTTCGACGTTCTTCCAGGAAAACGCATCCGGAGAGATTTGTTGTTTAAGGAATGCTCTG 1174
Db   1889 CACTTCTGGAACGAAAAGCATTCAAGAACAAATTTACAAAAATTATGTGAAGAGTAGCCG 1948

Qy   1175 GTTACTCGGAGGATGGTGAAATGGTGGTGAGGTGAAACGCATTTTGCATCACGCGATTC 1234
Db   1949 TTTATAATCACCAAATTGAAAAAGGTTACAAAGTGTTGAAATCGTTAAACGAAGCAAATTC 2008

Qy   1235 AGTCCACCATGGCGCGGTTAAAGGTGTGTCGGGTGGTAGTGATTCCTGTGTGATAATCGGCTAAGG 1294
Db   2009 GTACGGCATATGAACAAAAAGGTGTAGCCTGTTGTTGTTTCCTACGACTTATTAACTG 2068

Qy   1295 AAGACCCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCGCACTCCGTGGTGT 1354
Db   2069 AAAA---AATTAAAGATACAACGAATAAACCAGTAGATACAATCACAGACCAACACAGTAGTAT 2125

Qy   1355 TCCCGGATCCTACTGAGGCTCGCAGCGCGCTGGTCGGAGGCGGATTAACACGCTAAGTCTGTCA 1414
Db   2126 CACCAAAAAATATAAAGACATCAAAAAGCGGTTAAACTAATTAATAAAAGTAAAAAAGCCTG 2185

Qy   1415 CTTTGTTCTCGGGTCGCGGGGGTGAAGGAAATGCTCGCCGCGCGGTGTTGGGCGGAGA 1474
Db   2186 TCATGTTAATTGGTGTGTAGGGTCGGAAACATGCGAAAGATGACGTACGTGAATTTATTGAA 2245

Qy   1475 AGATTAAAATCACCGATCGGGGCCATGCGCTGGGGTGAAGCAGTACATCCAGCATGAGAATC 1534
Db   2246 TGGCTAAAATTCCTGTCATCATTACCAGCTAAAACAATCTTGCCGGATGATCATC 2305

Qy   1535 CGTTTCGAGGTCGGCATGTCTCGCCTCGCTTGGTTACGGCGCCTGGATGCGTCCAAATG 1594
Db   2306 CATATAGTATCGGTAACTTAGGTAAAAATCGGGTTACCAAAAACATTCTTATCAAAACAATGCAGG 2365

Qy   1595 AGGGCGGATCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTCGATTTCCTTCCTCAAAG 1654
Db   2366 AAGCCGGATTTATTAATTAATTATGGTTGGGTACAAAACTATCCATATGTGGATTACTTACCTAAGA 2425

Qy   1655 ACAACCTTGCCCAGGTCGGATAATCAACGGTGCCGCACATTGGTCGACGTACCACGGTGAAGT 1714
Db   2426 AAAAATATTAAAGCCATTCAAATTGACA-----CAAATCCTAAAAAATATCGGACATCGGTT 2479
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Qy   1715 ATCCGGGTGACCGGTGATGTGTTGCTGCGACAACAATCGAAAATAATTGCCCTCGTGAAGAAA 1774
Db   2480 TCAATATTAATGTATGAGAATTGTTGAGATAGTAAAAAATTGGCATCGAATTGAA 2539

Qy   1775 AAACAGATCGTTCCTTCCCTTGATCGGATGCT---CAAGGCACACGAGGCGTAAGTTGACTT 1831
Db   2540 ATATTAAACATGTTGCTGAAAGACCAATTCTTAAACAAAAACGTTAGAACGTAAAGCGTT 2599

Qy   1832 CGGTGGTGAGAGACGTACACACATTAACCTCGAGAGAGCATGTGCCTTATTCACCCTGAATACG 1891
Db   2600 GGGATAAAATGGGATGGAACAAAGATAAAAAATAATAAAGATAGTAAAAACCATTTAACGTCCAGAACCGAT 2659

Qy   1892 TTGCCTCTCTATTTTGAACGAGCTGGCGGCGGTGGGCGGTGGGTGTTTACTGTGTGGATGACCCGGCA 1951
Db   2660 TAATGGCATCAATCAATAAATTTATTAATAGATGATGCAGTGAGTGCATGCAGAGTAGGTA 2719

Qy   1952 TGTGCAAGTGTGGCATGCGAGGTACATCGGAGGAATCCGAGGCGGAAGCGCGCGGACTTTGTGG 2011
Db   2720 CAGCAACAGTTGGTCAACTCGATACTT---AAACCTTGGGTGTAAAATAACAAGTTCATCA 2776

Qy   2012 GTTCATTCCGCCACGGCACGGATGGCGTAAATGCGTTGCCTCATCGGATTGGTGCGGAAAGTG 2071
Db   2777 TTTCAAGTTGGTTAGGTGTACAAATGGGTTGCGGTCTTCCAGGTGCAATTGCATCAAAAATTG 2836

Qy   2072 TTGATCGAAAACCGCCAGGTGATCGGCGGATGGTGGGGCGGATGGGTTGGGCATGGCTGCTGG 2131
Db   2837 CATATCCAAATAGACAAGCCATCACGAAATTGCTCGGTGTGGGCAAATGGGTAAGC 2896

Qy   2132 GTGAGCTTCTGACGGTTAAGCTGCCACCCAACTTCCCGCTGAAGGCTGGTGTGTTTAACAACA 2191
Db   2897 AAGACTTCGGCTACAGCGAGCAGTACAACATAATCGAATTTACCTTTAAGTCGTATTTTGTACTTAATAACA 2956

Qy   2192 GTTCTTTGGGCATGGTGAAGTTGGAGAGTGTAAGAGTTTGGGAGGGACGGCAGCGAGAATTTGGGTACTG 2251
Db   2957 AACAGTTAGCATTTATTAATGAACAAGACAGCTGGTCGAAATGGTGAGTTG 3016

Qy   2252 ACCATGAGGAAGTGAATTTCGGCAGAGTAGACGTGCGGGGTATCAAATCGGCTAGGCA 2311
Db   3017 AATTTTCTGATATGGATCCATGCAAAAATTTTGTCTGAGCGAGCAGCGTGGTTATACAA 3076

Qy   2312 TCACCGGATCCGGAGAAGTTCCGCGAGCAGCTGACGTGGCATTGGCAGGTGGGGACCTG 2371
Db   3077 TTAAGAGTGCTAGCGGAAGTAGATGCTATAGTCGAAAGAGGCATTAGCACAAGAATGTACCAA 3136

Qy   2372 TACTGATCGACTATCGTCACGGAATCCTAAATGGCGTGTCGTGCTCCACCAACCATCACGTGGG 2431
Db   3137 CGATTGTAGATGTATATGTTGATCCTAATGCTGCGCCATTACCAGGTAAAAATTGTAAATG 3196

Qy   2432 AACAGGTCATGGGGATTCAGCAAGGCGGC 2459
Db   3197 AAGAACGCGCTTGGTTGTTATTGGTAAGTGGGC 3224
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'  SOFTWARE: ASCII Text
'  CURRENT APPLICATION DATA:
'     APPLICATION NUMBER: US/08/781,986A
'     FILING DATE:
'     CLASSIFICATION: 435
'  PRIOR APPLICATION DATA:
'     APPLICATION NUMBER:
'     FILING DATE:
'  ATTORNEY/AGENT INFORMATION:
'     NAME: Benson, Bob
'     REGISTRATION NUMBER: 30,446
'     REFERENCE/DOCKET NUMBER: PB248PP
'  TELECOMMUNICATION INFORMATION:
'     TELEPHONE: (301) 309-8504
'     TELEFAX: (301) 309-8512
'  INFORMATION FOR SEQ ID NO: 138:
'     SEQUENCE CHARACTERISTICS:
'        LENGTH: 7900 base pairs
'        TYPE: nucleic acid
'        STRANDEDNESS: double
'        TOPOLOGY: linear
'  US-08-781-986A-138

Query Match   45.0%;  Score 138.8;  DB 4;  Length 7900;
Best Local Similarity   4.3%;  Pred No. 2.1e-32;
Matches 741;  Conservative   0;  Mismatches 887;  Indels  20;  Gaps  5;

Qy     820 GAACAAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGGAATTTAGGTTGGTTGGGT  879
           |||||    ||||||| |||||   ||| ||||| |||   ||||||  |  || ||||||
Db    1589 GAAGCATTAGTTAAAGCATTACAAGCACTAGGGATATAGATCACTTGTATAGGGTATTCCAGGA 1648

Qy     880 GACAGCCTTAAATCGGATACGTGGATGTCGTTCCGGCCAATCAGATA------TTGAGTGGGTGC  934
           |||||||  |      | |||||||  || ||     |||       |||||| ||  |||||
Db    1649 GACTCAAATCGACGCATAGTCGATAGTTTACGGTACAGTGAGAGATCAAATTAAATTTTATC 1708

Qy     935 ACGTTCGAAATGAGGAAGAAGCGGGTGCGGAATCGTTGATCACTGGGG  994
           |||||   ||||  |||| || |||||||| |||  |||||||| |||
Db    1709 ATGTTACGTCATGAAGAAGTAGCAAGCTTAGCGGGCCCTGGTTTAATTCATTAAATTAACTGGTA 1768

Qy     995 AGCTGGGCAGTATGTGCTGCTTCTTGTGTGGTCCTGGAAACACACACTTGATTCGAGGTCTTTT 1054
           || || ||||  ||||| |    |||  | |||||  | |||  ||||| |||||| ||||||
Db    1769 AAATCGGTGTGCGCATTAAGTATCGGTTGGCCCTGGTTTAATTCATTTAATTGGTTATGT 1828

Qy    1055 ATGATTGCGCATCGAAAATGGGTTCGCGAAGGTGTGTTGGCCATCGCTACCGCATATTCCGAGTGCCC 1114
           ||||| |||||| || | ||  ||||||  || ||||| |  ||  ||  |||||  |||||
Db    1829 CACTTGGAACGAAAGCAATTCCAAGAAAACAAATTTACAGAAAATTATATCTGGACAAAAGTAGTACAG 1888

Qy    1115 AGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGAATGCTCTG 1174
           | |||||||  ||||  ||||||||||  | ||||||||  || |||
Db    1889 CACTTGGAACGAAAGCAATTCCAAGAAAACAAATTTACAGAAAATTATATCTGGACAAAAGTAGTACAG 1948

Qy    1175 GTTACTGCGAGATAGGTGATCGTGAATGGGTGAACCATTGCTGAGAGGTGAACCGATTC 1234
           |||  ||  |  |||| |||  |||  || |||| ||| ||  |||  || |  ||||
Db    1949 TTTATAATCACCAAATTGAAAAGGTGACAAATGTCTTTTGGAAAATGGTTAACGAAGCAAATTC 2008

Qy    1235 AGTCCAACCATGCGGCGGGTAAAGGTGTGTCCGGTGGTAGTGATTCCTGGTGATATCGGCTAAGG 1294
           |||   |||||  || ||||  || ||| |||| ||||| || || |||||||||  |  |||
Db    2009 GTACCGCAGGTGACGGCTACTTATTCCAATTCCACTATTCTTCTGTGTGGTGTT 2068

Qy    1295 AAGAGGCAGGTGACGGCTACTTATTCCAATTCCACTATTCTTCTGTGTGGTGTT 1354
           |||||||   | |  |||||    || ||  ||||||||  |  || ||||||
Db    2069 AAAA---AATTAAAGATACAACGAATAAACACTAGTAGATACAACAAGACCAACAGTACTAT 2125

Qy    1355 TCCCGGATCCTACTGAGGCGTGCAGCGCGGCTGGTGAGGGCGAAGTTCGTCTGTCA 1414
           ||| ||||  |||| |||  ||||| |  |||||||  |||||||||  |  |||
Db    2126 CACCAAAATATATAAGACATCAAAAAAGCGGTTAAACTAATTAATAAAGTAAAAACCCTG 2185

Qy    1415 CTTTGTTCTGCGGTGCGGGCGGCGGCCGTGAAGAAATGCTTCGCGCGCGTGAGGATTTGGGAGA 1474
           ||||||||| || |   |||||||||||||     | |||| |||  ||||| ||
Db    2186 TCATGTTAATTGGTTGTAGGTGCGAAACATGCAAAGATGACCTAGCTGAATTTATTGGGGGAGA 2245

Qy    1475 AGATTAAAATCACCGGATCGGGGCATGCGCTGGGGTGGTGGTAGCAGTACATCCAGCATGAGAATC 1534
           |||| |||   |  |  ||| ||  ||||  |  || || ||     ||    | |||||  | |
Db    2246 TGGCTAAAAATTCCTGTCATTCAATCATTCATTACCAGCTAAAAACAATCTTGCCGGATGATCATC 2305

Qy    1535 CGTTTGAGGTCGCATGTCTCGCCGGCCTGCTGGGTTCTTCGGGCCCTGCGGTTCTTGGGATCGATCATC 1594
           ||| |||| |  |||   ||| || ||| || | |  ||  |||   |||  |||  || || ||||
Db    2306 CATTAGTAGTATCGGTAACTTAGGTTAAAATCGGGTTACCAAAAACATCTTATCAAAACAATGCAGG 2365

Qy    1595 AGGCGGGATCTGCTCTGAATTCTATTAGTGGGTAACGGGTACGGATTTCCTTATTCTGAATTTCCTTCTTAAG 1654
           ||| ||| || || || ||  ||||||   || |||  | |||  |||  ||  || ||  ||   |  ||
Db    2366 AAGCGGGATTTATTAATTATGGTTGGTAACAAACTATCCATATGTGGGAATTACTTAACTGAAA 2425

Qy    1655 ACAACGTTGCCCAGGTGGCATATCAACGGGTGCGCACATTGGTTGCGACGTACCACGGTGAAGT 1714
           ||||||||   |||||||  |||| ||   || |||||| || || | ||||   | ||| |
Db    2426 AAAATAATTAAAGCCATTCAAATTGACA------CAAATCCTAAAATAATCGGGACATCGTT 2479

Qy    1715 ATCCGGTGACCGGTGAGTGTGCTGCGACAACATCGGAAAATAATTTTGCCTCATGTGAAGGAAA 1774
           || ||||| | || ||| | || |  | ||| |||      || |  |  | ||||| |  |
Db    2480 TCAAATTAATAGTAAGAATTGTTGGAGATAGTAAAAATTGGCGTTGCATCAGTTAACTGAAA 2539

Qy    1775 AAACAGATACGTTCCTTCCTTGATCGGATGTCGT---CAAGGCACACGAGCGTAAGTTGAGCT 1831
           ||||||| ||||  || ||| |||  ||||| |||   |||| ||| |||||||||| ||||
Db    2540 ATATTAAACATGTTGCTGAAAGACCATTCTTAAACAAAACGTTAGAACGTTAAAGCGGTTT 2599

Qy    1832 CGGTGCTAGAGACGTTACACACATAACGTCGGAGAAGCAATGTGCCTATTCACCCTGAATACG 1891
           |||| | || ||| | ||||| | || | | ||||||||  | || |||| ||   ||  ||
Db    2600 GGGATAAATGGAGTGGAACAAGATAAAAAATAAGTAGAGTAAAACCAATTACGGTCCAGAACGAT 2659

Qy    1892 TTGCCTCTATTTTGAACGAGCTGCGGATAAGGATCTAAGAAGAGCGGGTGTTTTACTGTGGGATAACCGGCCGCA 1951
           |||   |  ||  ||  || ||  |  | |  ||| ||| ||||||   |  || || || |||| ||||
Db    2660 TAATGGCATCAATCAATAAAATTATTTATTAAAGATACAAGAATGCAGTAGATTTCAGCAGGATGTAGGTA 2719

Qy    1952 TGTGCAAGTGTGTGGGCATGGGCAGGTGTACATCGAGAATCCGAGGGAACCGCGGACGACTTTGTGG 2011
           || || |||||  || ||| |||| | || || | || |||  |||| | |  |||| |||  |  |
Db    2720 CAGCAACACTTGGTCAACTCGATACTT---AAACCTTGGGTGTAAAATAAACAAAGTTCATCA 2776

Qy    2012 GTTCATTCGCGCCACGGGCACGATGGGTCAATGCGGTCAATGGTTCGGCTTCCGATTGGTGGCGCAAAGTG 2071
           |||||| |  | |  | |||| |||| ||   |||| |    | |  ||  | ||  ||||  || ||||||
Db    2777 TTTCAAGTTGGTTAGGTTGAACAATGGGTTGCGGTTCTTCCAGGTTGCAATTGCATCAAAAATTG 2836

Qy    2072 TTGATCGAAACCGCCAGGTGACGATGAGTGTGGCGGATGGTGGTTTGGGCATGTCGCTGG 2131
           ||||  || |  |||| |   ||||| || || ||| |||  |  |||||||| ||||||
Db    2837 CAATATCCAAATAGACAAGAAGCCCAATTGCTGGGTGGACGCGTGCAATTCCAAATGGTAATGC 2896

Qy    2132 GTGAGCTTCTGACGGTTAAGCTGCCACCAAACTTCGCGCTGAAGGCTIGTGGTTGTGTTACAACA 2191
           |||||| || |  || ||||| || ||||| ||| ||| |||| |   | || ||| | ||||
Db    2897 CATATCCAAATAGACAAGAAGCCCAATTGCTGGGTGGACGCGTGCAATTCCAAATGGTAATGC 2956

Qy    2192 GTTCTTTGGGCATGGTGAAGTTGGAGATGCTCGGTCGTGGAGGACAGCCAGAGAATTTGGTACTG 2251
           ||| |||  | |||||| ||| ||||||| || || |||||||| || |||||| ||||||
Db    2957 AACAGTTAGCATTTATTAATATGGCCATTCGAAGAGGCATTAGCACAGAGATGTACCA 3016

Qy    2252 ACCATGAGGAAGTGAAATTCCGCAGAGAATTGCGGCGCTGCGGGGTATCGGTACCGCA 2311
           |||| || |||||  ||||  | |||||| ||||| | ||    | ||||||  ||||
Db    3017 ATTTTCTGATATGGATCAAGCAAAATTGCTGGGACGCAGCGAGGCAGCACGGGTAAAGGTTATACAA 3076

Qy    2312 TCACCGGATCCGGAAGAAGAAGTTCGGCAGCAGCTAGCTGGCCATATCCTTGGACCTTG 2371
           ||  ||||||| |||| | |||| || |||| |||   |||| |||||| ||||  |||
Db    3077 TTAAGAGTGCTAGCGAAGTAGAATGCTATAGTCGGAAGCATTAGCACAGAGATGTACCA 3136

Qy    2372 TACTGATCGGATATCGTCACGGGATCCTAATGCGGCTGTGTCGATCCCACCAACCATCACGTGGG 2431
           || ||| |||| |||| |||| ||| ||||   | || ||| || |   || |||||||  |  |
Db    3137 CGATTGGTAGGATGTATAGTTGAATCCTAATGCTCGCGACCATTACCAGGTTAAAATTGTAAATG 3196

Qy    2432 AACAGGTCATGGAGTTCAGCAAGGCGGGC 2459
           ||||| || || |  |||||||||| |||
Db    3197 AAGAGCGGCTTGGTTATGGTAAGTGGGGC 3224
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;  RESULT 12
;  US-09-252-991A-7166/c
;  Sequence 7166, Application US/09252991A
;  Patent No. 6551795
;  GENERAL INFORMATION:
;     APPLICANT: Marc J. Rubenfield et al.
```

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; TITLE OF INVENTION:
; TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136         NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7166
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-7166

Query Match             4.0%;  Score 129.6; DB 4; Length 798;
Best Local Similarity  52.6%;  Pred. No. 3.6e-30;
Matches  307; Conservative   0; Mismatches 274; Indels   3; Gaps   1;

Qy   1856 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTTATTTTGAACGAGCTGG 1915
          |||| |||| | || ||  || |||  || |||||| || ||| || | | ||||| |||
Db    644 AAGCCGGCAAGGGCGAGCTGATCCATCCGCGACGACCTGGTCAGCCTGCTCGACCAGCACG  585

Qy   1916 CGGATAAGGATGCGGTGTTTTACTGTGGATACCGGCCATGTCGAATGTGTGGCATGCGAGGT 1975
          |||  | ||| | | ||  |  | || | |||  | || | | |||| || |||| || |
Db    584 CCAGCCAGGAGACGCCCTGTTCACCGCCGACGGCGGCCTCGGCGGATGGTTCTGGCGTTGCGTC  525

Qy   1976 ACATCGAGAATCCGGAGGAACGCGCCGACTTTGTGGGTTCATTCCGCCACGGGCACGGATGG 2035
          |||| || || || | || || ||  |  | | |||| |||| ||||| || || |  |||
Db    524 ACATCCACA---GCAACGGCAAGCCGCACCCTCACCAGCCTGGTCCACGGCACCATGG  468

Qy   2036 CTAATGCGTTGCCTCATGCGGATTGGTGTCGCGAAAGTTTGATCGAAACCGGCCAGGTGATCG 2095
          || ||  ||| || |  | ||||||| |||| | || | || |||||| ||| || || |||
Db    467 CCAACGCCATGCCCCCAGGCGCTGGGGCCGAGAAGGCCTACCCGAAGCCCAGGGTGATCT  408

Qy   2096 CGATGTGTGGCGATGCGTGGTTTGGGCATGCGGTGGTTGAGCTTCGACCGTTAAGCTGC 2155
          |||||||| | ||| | ||| || ||| || | ||| | || | | |||| |||||||
Db    407 CGATCTCCGGCGACGGCCGGCCATGCTGCTCGGCGACCTGCTGACCGGCCATCCAGG  348

Qy   2156 ACCAACTTCCGCTGAAGCCTGTGGTGTTTAACACACAGTTCTTTGGCATGGTGAAGTTGG 2215
          || ||||| ||| |||| | ||| | ||| |||| |||| ||| ||||| || | || |
Db    347 AAAAACTGCCGATCAAGGTAGTGGTTGCTGACAAATGCCTCGGCTGAACTTCGTCGACGTGG  288

Qy   2216 AGATGCTCGGTGGAGGGACAGCCAGGAATTTGGTACTGACCATGAGGAGTGGAATTTGCGCAG 2275
          || ||| ||| || || |  ||| | || | |||| | || ||| | | || ||| ||| |
Db    287 AACAGAAGGTGCGAGGGCCTGCTTGCTGGACAGCTACACCGACCTGCTCAACCCGACGACTTCGCCC  228

Qy   2276 AGATTGCGCGCGGCGCTGCGGGTGGTTGATCAAAATCGGTACGGCATCCGGACAGAAAGTTCGGCG 2335
          ||| || | | | | ||  || || | || ||| ||||| |||| |||| | || |||| |||
Db    227 GTCTCGCCCGAAGTGAGTGATCGGCTTCACCGAGCGCGGCTTCACGATGGCTTCGCAGGACTGGTGGCGA  168

Qy   2336 AGCAGCTAGGTGAGGGCAATTGGGCATTACCTTCGGGACCTGTTACTGGATCGGATATGCGTCACGGGATC 2395
          |||| ||| || | ||  ||||| || | | | |  ||||| |  ||| | || |  | |||| ||||
Db    167 CGGGGGTGCGAGGAGTTCCTCGCCCAGCCGACGGCCTTGCTCTGGAGCGGTGCCATACCAACC  108

Qy   2396 CTAATGCGCTGTCGATCCCAACCATCACGTGGGAACAGGTC 2439
          || ||| | ||||| |||| | ||||| |||| ||||| |
Db    107 CTGCGCGAGCTGGTGATGCGCCCGGAAGATCGAGTTCGGGCCCAGGTC   64
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RESULT 13
US-09-107-532A-3181
; Sequence 3181, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
;   APPLICANT: Lynn A Doucette-Stamm  and David Bush
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                       ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;   NUMBER OF SEQUENCES: 7310
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;     STREET: 100 Beaver Street
```

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;     CITY: Waltham
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02354
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: CD/ROM ISO9660
;     COMPUTER: PC
;     OPERATING SYSTEM: <Unknown>
;     SOFTWARE: ASCII
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/107,532A
;     FILING DATE: 30-Jun-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/085,598
;     FILING DATE: 14 May 1998
;     APPLICATION NUMBER: 60/051571
;     FILING DATE: July 2, 1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Ariniello, Pamela Deneke
;     REGISTRATION NUMBER: 40,489
;     REFERENCE/DOCKET NUMBER: GTC-012
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (781)893-5007
;     TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3181:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1746 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;   ANTI-SENSE: NO
;   HYPOTHETICAL: NO
;   ORIGINAL SOURCE:
;     ORGANISM: Enterococcus faecium
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: (B) LOCATION 1...1746
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3181:
; US-09-107-532A-3181

Query Match             3.4%;  Score 110.2; DB 4; Length 1746;
Best Local Similarity  44.2%;  Pred. No. 7.8e-24;
Matches  653; Conservative   0; Mismatches 803; Indels  21; Gaps   4;

Qy    914 AATCAGATATTGAGTGGGTGCACGTTCCGAAATGAGGAAGCGGGGCGGGTTTCAGCGCGTG  973
          || | ||||| ||| | |  ||| ||  |||| ||| || | | | |||| || |||| |
Db    137 AAACCGGAAATCAACTACATTCAAGTTCGTCATGAACAGAGAGTCGGCGACTCGGCACCGCCTG  196

Qy    974 CGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCGAAACTGGCGAAAGCTCGTGGGTTCGGAAACA 1033
          | ||| |||||| |||| |||| |||| ||| |||| |  | || || |||| |  ||||||||
Db    137 CAGATGCAAAATTACGGGGAAAAGTCGGCCGTTGTCTTCGGCTTCTTGTGGTTCCTGGAAACA 1033

Qy   1034 CACACCTGATTCAGGGTCTTTATTGATTCGCATCGAAATGGTCGAAGGTGTTGGCCATCG 1093
          | ||| ||| |  |||| | ||  ||| | || | | |||| ||| | | || ||||
Db    197 CAGATGCAAAATTACGGGGAAAAGTCGGCCGTTGTCTTCGGCTTCTTGTGGTTCCTGGAAACA 1033

Qy   1094 CTAGGCATATTCCGAGTGCCCAGATTGGTTCGGACGTTCTTCCAGGAAAACGCATCCGGAGA 1153
          || || | |  || | | || | |  | | || | |||| |||| |||| | |||||| |
Db    257 CACATTTGATCAAATGGTTTGTATGATCGACAGATGGACCATGTGCCTCTAGTAGCCGTTCT  316

Qy   1154 TTTTGTTTAAGGAAATGCTCTGGTTACTGCGGAGATGGTGAATGGTGGTTGAGCAGGGTGAAC 1213
          || | |||| || | ||| | ||| | | | || || | || | | ||| | ||| || |
Db    377 CTATTTTCGCAGATGTTAGCGTATACAATCGTCAGTCATGACACCACACAAAGTCTTCGC  436

Qy   1214 GCATTTGCATCACCGGATTCAGTCCACCATGGCGCGGGTAAAGGTGTGTCGGTGGTAGTGA 1273
          | || ||| || | |||| | || ||| | | | |||| ||||| |||| |||| |||
Db    437 ATGTAGTAGATGAAGCCATTAAAGCCGCCTATGAGCATAAAAAGGCGTGGGCTATCGGTGACTA  496

Qy   1274 TTTCCTGGTGTATATCCGCTAAGGAAGACGCGACGGTACTTATTCCAAATTCCACTATATTT 1333
          |||| | | | ||| | ||||| ||  | | || || || || | || |||| |||| ||
Db    497 TCCCGTTGATCTTGGTTGTTTTCAAGAAATTGACGAACAACCTTTCTCCA---CCGGTCACA  553
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RESULT 14
US-09-134-001C-1619
; Sequence 1619, Application US/09134001C
; Patent No. 6380370
GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1619
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1619

Query Match   43.6%; Score 101.6; DB 3; Length 1761;
Best Local Similarity   3.1%; Pred. No. 4e-21;
Matches 721; Conservative   0; Mismatches 904; Indels 27; Gaps 5;

[The remainder of this page consists of a nucleotide sequence alignment (Query "Qy" versus Database "Db") presented in a rotated two-column format, showing paired sequence rows with positional numbering and alignment match bars.]

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8458
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8458

Query Match   45.5%; Score 100.4; DB 4; Length 2577;
Best Local Similarity 45.5%;
Matches   773; Conservative 0; Mismatches 856; Indels 69; Gaps 9;
              Pred. No. 1.2e-20;

[Nucleotide sequence alignment between Query (Qy) and Database (Db), aligned in paired rows with position numbers flanking each segment]

```
Db  1585 CTCGGACCCGCGCCAGCACGATGCTGATGGAGCATTGCGACACCCTGCTGATCGTCGGC 1644
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1621 ACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTTGGATATCAAC 1680

Db  1645 AGCACTTTTCCCCTACAGCGAGTTCCTTACCCAAGGCCGCGGGGGGGGCGGTGCAGATC 1704
         |||
Qy  1681 GGTGCG------------CACAATGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGAT 1731

Db  1705 GACCTGTATCCGCGCAACATCGGTATCCGTATCCGGATCCGACCAGGCCCTTGCTCGGCGAT 1764
         |||
Qy  1732 GTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAGGAAAAAAACAGATCGTTCCTTC 1791

Db  1765 GCAGGGGAAACCCTGGAGCCCGCCCTGCCTGCTCGACGCAGAAAAACCACGCGCCCT-- 1822
         |||
Qy  1792 CTTGATCGGATGCTCAAGGCCACACGAGCGTAAGTTGAACGTCGGTGGTTAGAGACGGTACACA 1851

Db  1823 -------GGGCCCGCCGGGTCGAGCGGGGGGGGTGACGGGCCAGTGGGCAGGAAGCCCCGGCGC 1875
         |||
Qy  1852 CATAACGTCGAGAAGCATGTGCCTATTCACCCTGAAATACGTTGCCTCTATTTTGAACGAG 1911

Db  1876 CAGGCCGAAGAGCCAGCCGACCCGACCCGATCAACCCGCAGCGGGTATTCCGTTCCTTGTCGGAG 1935
         |||
Qy  1912 CTGGCCGGATAAGGATGCCGGTGTTTACTGTGGATACCGGCATCGTGCAAATGTGTGGCAATGCG 1971

Db  1936 CAACTGCCGGACGATGCGATTCTCTGCGCGGACGCGGGCTCCGCATACCAACTGGTACGGCC 1995
         |||
Qy  1972 AGGTACATCGAGAATCCGGAGGGAAACGCGGCGACTTTGTGGGTTTCATTCCGCCACGCGCACG 2031

Db  1996 CGGGCACATCCGGCATGCCCGGGGGGGGGTTGAGGCCGCCAGTGGGCGGAGGAAGCCCGGCGC---TCGGGCAAGCTGGGCGACC 2052
         |||
Qy  2032 ATGGCTTAATGCCGTTGCCTCATCGGATTGGTGCGGCAAAGTGTTGATCGGAAACGCCAGGTG 2091

Db  2053 ATGGGCAGCGCGGCGGTGCCCTACCGGCATCGCCAAGCTCGCCTATCCGCAGCGGCGCGGTG 2112
         |||
Qy  2092 ATCGCGATGTGTTGGCGCAATGGTGGTTGGGGCCATGCTGCTGGGGTGAGCTTCTGACCGTTAAG 2151

Db  2113 GTGGGCGGATGGTCGGGCGACGGCGCCCATGCAGATGAACGCCGAACTGGTCACCCGTG 2172
         |||
Qy  2152 CTGCCACCAACTTCCGC-----------TGAAGGCTGTGGGTGTTTAACAACAGT 2193

Db  2173 CAGCAGTACTCGGCAGCCTGCGGACTCGCCGACCTTCATCGTGCTGGGTGTGCTGAACAACGGC 2232
         |||
Qy  2194 TCTTTGGGCATGGGTGAGAGTTGGAGATGC---TCGTGGAGGGACAGCCCAGAATTTGGGTTACT 2250

Db  2233 GATCTCAACCAGGTGACCTGGGACGCAGCGTGCCCTGGCCCGGCGACCCGGAGTTCAGCCCG 2292
         |||
Qy  2251 GACCATGAGGAAGTGAAATTCGCAGAG-------AATTGCGGCGGCCTGCGGGTATCAAAATCG 2304

Db  2293 GCGCAGGAAGTGATCGATTTCCCCTACGCCGGTTATGCGGACAATGCTCGGTTCAAGGGC 2352
         |||
Qy  2305 GTACGGCCATCACCGATCCGAAGAAAGTTCGCGAGCAGCTAGCTGAGGCAATGGGCATATCCT 2364

Db  2353 ATCCGCGTTGGAATCGGCCCCGGAGGACATCGACGCGCCGCCCTGGGCCCGAGGGCCTTCGCCGCCGAC 2412
         |||
Qy  2365 GGACCTGTACTGATCGGATATCGTCACGGGATCCTAAATGCGGCTGTTGCATCCACCAACCATC 2424

Db  2413 CGCCCGGTGCTGCTGGAGGTGGTCACCGACACCCGAACGTGCCGCGGCGCGCCGCACATC 2472
         |||
Qy  2425 ACGTGGGGAACAGGTCATG 2442

Db  2473 AGTTTCGGAGCAGGCCAAG 2490
         |||
Qy  2473 ACGTGGGAACAGGTCATG 2442
```

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: January 15, 2005, 07:17:41 ; Search time 169.349 Seconds
                 (without alignments)
                 9065.911 Million cell updates/sec

Title: US-09-965-825-1
Perfect score: 2160
Sequence: 1 ttagagggcgattctgtgagg..............ggtgcccatgagagattgccct 2160
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	366.2	17.0	1746	4	US-09-543-681A-4139	Sequence 4139, Ap
2	362.8	16.8	1749	4	US-09-489-039A-4884	Sequence 4884, Ap
3	305.2	14.1	1719	4	US-10-096-571-1	Sequence 1, Appli
4	269.4	12.5	1737	4	US-09-252-991A-7335	Sequence 7335, Ap
c	5	227.4	10.5	1293	4	US-09-489-039A-4905	Sequence 4905, Ap
c	6	164.2	7.6	1083	4	US-09-252-991A-7413	Sequence 7413, Ap
c	7	164.2	7.6	1113	4	US-09-252-991A-7281	Sequence 7281, Ap
c	8	155	7.2	1454	4	US-10-096-571-7	Sequence 7, Appli
c	9	152.8	7.1	1448	4	US-10-096-571-8	Sequence 8, Appli
10	138.8	6.4	7900	4	US-08-781-986A-138	Sequence 138, App
11	138.8	6.4	7900	4	US-08-956-171E-138	Sequence 138, App
12	129.6	6.0	798	4	US-09-252-991A-7166	Sequence 7166, Ap
c	13	110.2	5.1	1746	4	US-09-107-532A-3181	Sequence 3181, Ap
14	101.6	4.7	1761	3	US-09-134-001C-1619	Sequence 1619, Ap
15	100.4	4.6	2577	4	US-09-252-991A-8458	Sequence 8458, Ap
16	100.4	4.6	2754	4	US-09-252-991A-8530	Sequence 8530, Ap
17	87.2	4.0	260	3	US-08-735-545-24	Sequence 24, Appl
18	87.2	4.0	260	3	US-09-449-083-24	Sequence 24, Appl
19	81.2	3.8	1443	4	US-09-252-991A-8318	Sequence 8318, Ap
20	68.8	3.2	2111	4	US-10-096-571-11	Sequence 11, Appl
21	68.8	3.2	2111	4	US-10-096-571-13	Sequence 13, Appl
22	61.4	2.8	1776	4	US-09-583-110-152	Sequence 152, App
23	60.8	2.8	2841	2	US-08-452-075-1	Sequence 1, Appli
24	60.8	2.8	2841	3	US-09-231-061-1	Sequence 1, Appli
25	60.8	2.8	2841	4	US-09-011-762-5	Sequence 5, Appli
26	59.8	2.8	25002	4	US-08-961-527-48	Sequence 48, Appli
c	27	59.8	2.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	28	58	2.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
29	57	2.6	1689	4	US-09-489-039A-840	Sequence 840, App
30	55.8	2.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
31	55.8	2.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
32	55.8	2.6	1830121	4	US-10-329-960-1	Sequence 1, Appli
c	33	53.4	2.5	3390	3	US-09-550-338-1	Sequence 1, Appli
34	53.4	2.5	3390	3	US-09-767-878-1	Sequence 1, Appli
35	50.6	2.3	1701	4	US-09-583-110-1223	Sequence 1223, Ap
36	50.6	2.3	6211	4	US-08-961-527-8	Sequence 8, Appli
37	49.4	2.3	1947	1	US-08-489-039A-3367	Sequence 3367, Ap
38	49.4	2.3	2365	3	US-09-363-208-1	Sequence 1, Appli
39	49.4	2.3	2365	3	US-09-137-478-1	Sequence 1, Appli
40	48.6	2.2	1800	4	US-09-252-991A-3891	Sequence 3891, Ap
c	41	48.6	2.2	1824	4	US-09-252-991A-4025	Sequence 4025, Ap
42	48.6	2.2	1875	4	US-09-489-039A-3919	Sequence 3919, Ap
43	48.4	2.2	1689	4	US-09-489-039A-219	Sequence 219, Appli
44	48.4	2.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli
45	48.4	2.2	1664976	4	US-09-692-570-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-543-681A-4139
; Sequence 4139, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI;
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4139
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4139

Query Match   17.0%;   Score 366.2;   DB 4;   Length 1746;
Best Local Similarity   53.7%;   Pred. No. 3.2e-108;
Matches 899;   Conservative 0;   Mismatches 758;   Indels 18;   Gaps 6;

Qy   374 AGGTGTGAAGGGAATTTATGGTTTGGTTTGGGTTGACAGCCTTAATCCGATCGTGGGATCCTGT 433
           ||||| ||||||||||||||||| |||||| |||| |||||| ||| ||||||| |||||||
Db   72 AGGTGTGAAAAGGTATTTGGGGGTGACGGGGCGGATCATTGAAATGAAATGAATTAAGTAGATAGCTT 131

Qy   434 CCGCCAAATCAGAT---ATTGAGTGGGTGCACGTTCGAAATGAGGAAGACGCGCGGCGTTTTGC 490
           ||| || ||| ||| | |||||||| |||| ||||||||||||||| || |||| |
Db   132 GCGCAAAATGGGTACCCATTGAAATGAATGGGCACACGCCATGAAGAAGTCGCGGCTTTTTGC 191

Qy   491 AGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCCAGTATGGGCGTGCTTGCTTGTGGTCC 550
           || |||| | || ||||| ||||| |||| | |||| ||||||| | ||| || ||||||||
Db   192 CGCCGGAGCAGAAGCGGCTATCAATGGGTAATTAGCGGTTTGTTGTGCGGGCGTCCCTGTGGACC 251

Qy   551 TGGAAACACACCTCGATTCAGGGGTCTTTATGATTCGCATCGAAATGGTGGAAGGTGTT 610
           ||||| ||||| || ||||||||||| ||||||||||| || ||||||||||||||||
Db   252 AGGTAACTTACACTTAATTAAATGGACTTTTTGATTGTGTCATCGTAGTTCCCGTGTT 311

Qy   611 GGCCATCGCTAGCCATCATTATTCCGAGTGGCCACCGGATTGGTTGCGACGTTCTTCCGGAAACGCA 670
           |||||||||| ||| ||| ||||| ||||||||||| |||||| |||| ||||||||||
Db   312 AGCGATTGCCCGCTCATTATTCCCTCTCGCTGAAAATGGTAGTTGAATGGTCAAGGAAACTCA 371

Qy   671 TCCGGAGATTTTGTTGTTTAAGGAAATGCTTCTGGTTACTGCGAGAATGGTGAATGGTGGTGAGCA 730
           |||||||||| |||| ||||||||| || |||| ||||| |||||||||||||||||||
Db   372 TCCTCAAGAGTTATTTCGTGAAATGAAGTGAGTCACTATCGTGAATTAGTCTTAATTCCCGATCA 431

Qy   731 GGGTGAACGCACATTTTGCATCACGCGATTCCACCATCGCGGGGTAAAGGTGTGTCGGT 790
           ||||| ||||| |||| |||||
Db   ...

US-09-543-681A-4139

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Db        432 GATCCCACAAATTCTGGCTATCGCTATGCGCACCGCTATTTGAAAAAGGGTGTTGCGGT 491

Qy        791 GGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTC 850
Db        492 GGTGGTATTACCCGGTGATGTAGCGTTAAAACCCGCTCCAGAAGATGCCCATGAAAATT- 550

Qy        851 CACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCAGCGCTGGT 910
Db        551 --GGTATCCACTACAATCACCACTGATTATGCCGAATCGTTTTGAAATCGAAAAACTGTC 608

Qy        911 GGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAGAATGC 970
Db        609 TGAGGCACTGAATAACGCTAAAAATATCACCTTAATGTGTGGTGCCGGTTGTGCTCAAGC 668

Qy        971 TCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCGCTGGG 1030
Db        669 ACATGATGAAGTGGTGAAACTAGCACAAACCTTAAAAGCCCCTGTTGTGCATGCACTACG 728

Qy       1031 TGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTGGCCTGCTTGG 1090
Db        729 TGGGAAAGAGTATCTTGAGTGGAATAATCCATGTAGCGTGGGAATGACGGGTCTTATCGG 788

Qy       1091 TTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTATTGGGTACGGA 1150
Db        789 TTTTTCATCGGGTTATCACGCAATGGAGAATGCCGATACTTTAGTGCTGTTAGGTACTCA 848

Qy       1151 TTTCCCTTATTCTGATTTCCTTCCT---AAAGACAACGTTGCCCAGGTGGATATCAACGG 1207
Db        849 ATTCCCTTATCGCGCTTTCTATCCTGCCAAAGCTAATATTATTCAAATTGACCTTAATCC 908

Qy       1208 TGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCAAC 1267
Db        909 AAGTAGTATTGGCTCACATTGCCATGTGGATATGGCTTTTGTTGGAGATGTCAAAGCAAC 968

Qy       1268 AATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGAT 1327
Db        969 CCTTAATGCATTACAACCGCGATTAAAAGAGAAAACAGATACCGCACATCTTGATGCCTC 1028

Qy       1328 GCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTCGA 1387
Db       1029 GTTAAA---ACATTATGCTAAAGCACGCAAAGATTTAGATGCATTGGCTCAACCTAGTG- 1084

Qy       1388 GAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGATAA 1447
Db       1085 --AGCGTGAGTTGATCCACCCTCAGTATTTAGCACGTCGATTAAGTGAATTAGCCAACGA 1142

Qy       1448 GGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGTACATCGA 1507
Db       1143 TGATGCGGTATTTACCTGTGATGTTGGCACGCCAACAGTTTGGGCAGCACGTTA---CGT 1199

Qy       1508 GAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGGCTAATGC 1567
Db       1200 GAAAATGAATGGTAAACGTCGTTTAATTGGTTCATTTAACCATGGCTCAATGGCGAATGC 1259

Qy       1568 GTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATGTG 1627
Db       1260 GATGGCGCAAGCTATTGGTATTCAAGCACTGGACAGAAAACGTCAAGTTGTGGCGATGTG 1319

Qy       1628 TGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAACT 1687
Db       1320 CGGTGACGGTGGTTTTACCATGTTAATGGGTGATTTCATCTCATTGGCTCAAATGAACTT 1379

Qy       1688 TCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATGCT 1747
Db       1380 ACCGGTGAAAGTGGTGATTTTTAATAACAGCGTATTAGGTTTTGTGGCGATGGAAATGAA 1439

Qy       1748 CGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAGAGATTGC 1807
Db       1440 AGCGGGGGGCTATTTGACTGATGGCACCGATTTACATAATCCTGATTTTGCCGCTATTGC 1499

Qy       1808 GGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCGAGCAGCT 1867
Db       1500 CAATGCGGCGGGAATTAAAGGTATTCGCGTTGAGAAAGGCGAAGATCTTGATGAAGCATT 1559

Qy       1868 AGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATCCTAATGC 1927
Db       1560 AAAAACAGCCTTTGAACATGATGGCCCTGTTATTGTGGATGTGGTAACCGCAAAACAAGA 1619

Qy       1928 GCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGGCGGCCAC 1987
Db       1620 GCTTTCCATGCCTCCGGAAATTAAATTTGAGCAGGCCAAAGGTTTAGCTTGTATATGAT 1679

Qy       1988 CCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGATCTGGCCCGTTCGAAC 2042
Db       1680 GAAAGCGATTATTAATGGTCGTGGCGATGAAATAGTGCAATTAGCGAAAACCAAC 1734

RESULT 2
US-09-489-039A-4884
; Sequence 4884, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 4884
;   LENGTH: 1749
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4884

  Query Match             16.8%;  Score 362.8;  DB 4;  Length 1749;
  Best Local Similarity   52.8%;  Pred. No. 4.1e-107;
  Matches  909;  Conservative    0;  Mismatches  792;  Indels   21;  Gaps    5;

Qy        327 ATGGCACACAGCTACGCAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 386
Db         31 ATGAAACAGACCGTGGCGGCATACATTGCCAAAACGCTGGAACAGGCCGGCGTGAAACGT 90

Qy        387 ATTTATGGTTTGGTGGGTGACAGCCTTAAT---CCGATCGTGGATGCTGTCCGCCAATCA 443
Db         91 ATCTGGGGCGTCACCGGAGATTCCCTCAATGGATTGAGCGATAGCCTTAACCGCATGGGC 150

Qy        444 GATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAA 503
Db        151 ACCATCGACTGGATGCCCACCCGGCACGAAGAGGTCGCCGCTTTCGCCGCTGGCGCGGAA 210

Qy        504 TCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACAC 563
Db        211 GCGCAGCTGACCGGCGAGCTGGCGGTCTGCGCCGGCTCCTGCGGACCGGGCAACCTGCAC 270

Qy        564 CTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGC 623
Db        271 CTGATTAACGGTTTGTTTGACTGTCATCGCAACCATGTCCCGGTGCTGGCCATCGCCGCC 330

Qy        624 CATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTG 683
Db        331 CACATCCCATCCAGCGAAATCGGCAGCGGCTATTTTCAGGAAACCCATCCTCAGGAGCTG 390

Qy        684 TTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATT 743
Db        391 TTCCGCGAGTGCAGCCATTACTGCGAACTGGTCTCCACGCCGGAGCAGATCCCGCAGGTG 450

Qy        744 TTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCT 803
Db        451 CTGGCAGTGGCGATGCGTAAGGCAGTGATTAACCGCGGCGTCTCGGTGGTGGTGTTGCCC 510

Qy        804 GGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCT 863
Db        511 GGCGATGTGGCGCTGAAGGCCGCCCCGGAAAGCGCCAGCAGCCACTGGTATCATGCGCC- 569
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Qy    864 GGCACTTCCTGTGTTGTTCCCGGATCCTTACTGAGGCTGCGTGGAGGCGGATTAAC 923
          |||||| |||   |||  ||||    ||||||||| |||||||||||||  |||||
Db   1941 CCAACCATCACGTTGGGGAACAGGTTCATCGGGATTCAGCGAAGGCGGCGCCACCCGAACCGTCTTT 2000

Qy    570 --GCTGCGAGGGTCACCCGGCGGGAGAAAGAGCTGGCGGCAAGCTGCGGATTATTCGC 627
          |||||||||||||
Db   1636 CCGCAGATCAAGCTGGGACGGAGCAGCCCAAAGGCTTTAGCCTGTGTATATGCTGCGGGCGGATCATC 1695

Qy    924 AACGCTTAAGTCTGTCACTTTGTTCTTCTGCGGTGCGGTGGCGGGTGAGAGAATGCTCGGCGCGAAGGTG 983
          |||||||||||
Db   2001 GGTGGAGGAGGTAGGAGGCGGATAATCGATCCGGTTGCGGAGCTCAAGGGGGGATCAAC 2042

Db   1696 AGCGGGCGCGCCGGGATGAGGGTCATCGGAACTGGGCGAAAACCGAAC 1737

Qy    984 TTGGGAGTTGGGGGAGGAAGAATTAAAATCACCGGATCACGGGGGCATGCGGCTGGGGTGGTAAGCAGTAC 1043
Db    688 GTGGGAGTTCGGCAGCCAAAAATTAAAGCCCGGGAAAGGGCGCGCCTGCCCGGCGAAAGAGCAC 747

Qy    628 TACTCCAGCAATATCCGCTCATGTCGGCAGCGGTTGGCGGCGCGCCACCAGAGAACTG 687

Qy   1044 ATCCAGCATGAGAATCCGTTTTGAGGTTCGGCAGTGTCTGGCCTTGGTTACGGGCGCCTGC 1103
Db   1044 GTGGAGTTACGGACAACCCGTACGGATGTGGGGGATCAGCAGGTTCTATTGGGGTTACGGGCGCCTGC 1103

Db    748 GTGGAGTTACGGACAACCCGTACGGATGTGGGGGAT...

RESULT 3
US-10-096-571-1
; Sequence 1, Application US/10096571
; Patent No. 6623944
; GENERAL INFORMATION:
;   APPLICANT: RIEPING, MECHTHILD
;   TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts th
;   FILE REFERENCE: 211499
;   CURRENT APPLICATION NUMBER: US/10/096,571
;   CURRENT FILING DATE: 2002-03-14
;   PRIOR APPLICATION NUMBER: DE 10112102.4
;   PRIOR FILING DATE: 2001-03-14
;   PRIOR APPLICATION NUMBER: US 60/304,776
;   PRIOR FILING DATE: 2001-07-13
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 1
;   LENGTH: 1719
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1716)
;   OTHER INFORMATION:
US-10-096-571-1

Query Match     14.1%;  Score 305.2;  DB 4;  Length 1719;
Best Local Similarity   50.7%;  Pred. No. 2.2e-08;
Matches  873;  Conservative   0;  Mismatches 828;  Indels  21;  Gaps   5;
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Qy    327 ATGGCACACAGCTACGCAGAGACAAGTTAAATTGACACTTTGGGAGCTCAAAGGTGTGAACGGA 386
Db      1 ATGAAAACAAACGGTTGCAGCTTATATCGCCAAAACACTCGAAATCGGAGGGA 60
Qy    444 GATATTGAGTGGGTGCACGTTCGAAATGAGAGAAGAGCGCGCGGGGCCTTTGCAGACCGTGCGGA 503
Db     61 ATCTCGGGGAGTCACAGCGCGACTCTCTGAAACCGTTCAGTTGGACAGTCTTAATCGCATGGGC 120
Qy    504 TCGTTGATCACTCGGGGGAGCTGGCAGTAATGTCGCTGCTTCTTCTGTGGGTCTCCGAAAACACAC 563
Db    121 ACCATCGAGTGGATGGGATTCACCCGCCACGAAGAGAGTGGCGCGGGCCTTTGCCGCTGGAA 180
Qy    387 ATTTANGTTCGGGGTGGGTGACAGCCTTAA---TCCGATCGTGGATGCGATCGGCAGCGGG 443
Db    181 GCACAACTTAGCGGAGAAGAACTGCGGTCGGCGGATCGTGCGCGGACCCTCCAC 240
Qy    564 CTGATCAGGGTCTTTATGATGAATGGTTCGCGCCCGGGTGGGCCATCGCTAGC 623
Db    241 TTAAATCAACCGCCTGTTCGAGTTGCCACCGCAATCACGTTCCGGGAAAGGCGAGATTTG 300
Qy    624 CATATTCGGAGTGCCCAGATTCGGTTCGGACGTTCTTCCAGGAAACGCATCCGGAGACTA 683
Db    301 CATATTCCCTCCAGCGAAAATTGGCACGGGCCTATTTCCAGGAAACCCCACAGAGCTA 360
Qy    684 TTTAAGGAAATGTCTCGGTTACTGCGAGATGTGAAGTGGTGAGAGCAGGGTGAACCCATT 743
Db    361 TTCCGCGAATTGAGTCACTATTGCGAGCTGGTTTCCAGCCGGTAAAGGTCGCAGCGATTCCT 420
Qy    744 TTGCATCACGCGATTCAGTCCACCATGGCGGGGTAAAGGGTCCCGAGACGTACTCCACAAGTA 803
Db    421 CTGGCGATTGCCATGCGCAAAGCGGTGCTTAATCACGTGGGGTGGTGGTTAGTGGTTACCA 480
Qy    804 GGTGATATCGCTAAGGAAGACCCAGGTGACGGTACTTATTCCACTATTTCTTCT 863
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Qy   481 GGCGACGTGGCGCGTTAAAAACCTGCGCCACGAGAGGGGC---AACCAATGCACGTGGCGG 537
Db
Qy   864 GGGCACTCCCTGCTGGTTCCCGGGATCCCTACTGCAGGCGTCGCTGAGGCGCGGCATTAAC 923
Db
Db   538 CCACAAACCACTGCGTCACTGCGAGAGAAGGAGTTACGCGAGGACGGCAAACTGCTGGCT 597
Qy
Qy   924 AACGCTAAGTCGTCGTCACTTTGTTCTGCGGCGGTGAAAGATGCTCGCGCGGCCAGGTG 983
Db
Db   598 TATTCCAGCAATATCGCCCTGATCGTGTGGCCAGCCGGCCGCGCGGGGGGGCGCATAAAGAGTTA 657
Qy

Qy   984 TTGGAGTTGGCGGACGAGAGATTAAAATCACCGGATCTGGCGGGCGTGGAGTCAAGAGTAC 1043
Db
Db   658 GTTGAGTTTTGCCGGGGAAAAAATTAAAGCGCCTTATTTGTTCAGCGCCTGCGCGGGTAAAGAACAT 717
Qy
Qy 1044 ATCCAGCAATGAGAATCCGTTTTGAGGTCCGCACGTCTCGGCCTGGTTACGGCGCCCTGC 1103
Db
Db   718 GTCCGAATACGGATAATCCGTTATCGGCTTCTCGGTCAGGT 777
Qy
Qy 1104 GTGGGAATGGCTCCAATGAGGCGGGATCTGCCTGGGTACGGGATTTCCCTTATTCT 1163
Db
Db   778 TTCCATACCATGATGAACGCCCGACACGTTAGTTGCTACTCGGCGACGCAAATTCCCTACCGC 837
Qy
Qy 1164 GATTTCCTTCCTA---AAGACAACAGTTCCCCAGGTGCATCAAACGTTGCCGCACAATTGGT 1220
Db
Db   838 GCCTTCTACCCGACCGATAGCCAAAATCATTCAGATTGAATGATAATCAAACCCAGCCATCGGC 897
Qy
Qy 1221 CGACGTACCACGGTGAAGTATCCGGTGACCGGCTGATGTTGCTGCAACAATCGAAAATATT 1280
Db
Db   898 GCTCACAGCAAAGGTGGGATATGGCACTCGCTCGCGCGATATCAAGTCGACTCTGCGTGCATTG 957
Qy
Qy 1281 TTGCCTCATGTGAAGGAAAAAAACAGATCGGTTCCTTCCCTTGATCGGATGCTCAAGGCCACAC 1340
Db
Db   958 CTTCCATTGGTGTGGAAGAAAAAGCCGAGAAAAATTGTCTGGATAAAGCGCTGGAAGAATTAC 1017
Qy
Qy 1341 GAGCGTAAGTTGGAGCTCGGGTGCTGGTAGGACGTTACACACATAAACGTCGAGAAGCATGTGCCT 1400
Db
Db 1018 CCGGACCGCCCGGCCAAAGGGCTGGACGATTTGACTAAACCGACCG------------AGAAAGCC 1068
Qy

Qy 1401 ATTCACCCTGAATACGTTGCCTCTCTATTTTGAACGACTGGCGGGATAAGGCGGTGTTT 1460
Db
Db 1069 AATTCACCCGCAATATCTGCGCAGACAAATTAGTCATTTGCGCCGCATGACGGCTATTTTC 1128
Qy
Qy 1461 ACTGTGGGATACCGGACATGTCAAGTGTGTGGCATGGCATCGGAGAATCCCGGACGGGA 1520
Db
Db 1129 ACCTGTCGACGTTGGTACGCCAAACGGTGGTGGGCGCACGGTTATCT---AAAAATGAAACGGC 1185
Qy

Qy 1521 ACGCGCCGACACTTTGTTGTGGGTTCATTCCGCCACGCAGCGGATGGCTAATGCGTTGCCTCATGGG 1580
Db
Db 1186 AAGCGTCGCCCTCGTTAGGTTCGTTTAACCACGGTTCGATGGCTAACGGCGCATGTCGCGCAGCG 1245
Qy
Qy 1581 ATTTGGTGCCGCAAAGTGTTGATCGAAACGCGCGGCCCAGGTGAGTGTGGGGTCTTTA 1640
Db
Db 1246 CTGGGCGTGCCGCAGGCGACACGAGCCGCTTCAGGTGGTCGGCGATGTGTGGCGATGGTGGT 1305
Qy
Qy 1641 TTGGGCCATGCTGCTGGGGTGAGCTTCTGACCGTTAAGCTGCACCACAACTTCCGCGCTGAAGGCT 1700
Db
Db 1306 TTTACCATGTTGATGGGCGCAGTTCCTCTCAGTAGTGCACCACAACTTCCGCTGAAAATT 1365
Qy
Qy 1701 GTGGGTGTTTAACACAGTTCTTTGGGCATTGGGAAGTGTGGGAAGGGACGGCACG 1760
Db
Db 1366 GTCGTCTTTAAACAACGCGTGCTGGGCCTTGTGTGCGATGGAGAATGAAAGCTGGTGGCTAT 1425
Qy
Qy 1761 CCAGAAATTTGGTACTGAGGAAGTGAATTGCGGCAGAGATTGGGAAGTGTGGTGAAACGCTGCTGGCA 1820
Db
Db 1426 TTGACTGAGGCACCGACTACACGACAAACTTTGCCGGGCCATTGCCGGCCGAGACGTGCGGGGT 1485
Qy
Qy 1821 ATCAAATCGGTACGGCATCACCGATCCGGAGAAAGTTCCGCAGAACGCTAGCTGAGGCATTG 1880
Db
Db 1486 ATTACGGGGTATCCGTGTAGAAAAAGCGTCTGAAGTTGATGAAGCCCTGCAACGCGCCTTC 1545
Qy
Qy 1881 GCATATCCTGGACCTGTACTGATCGATCGTAAATCGCGCTCGGATCCCA 1940
Db
Db 1546 TCCATCGACGGTCCGGTGTTGGTCGCCAAAGAAGAGAGTTAGCCAATTCCA 1605
Qy

RESULT 4
US-09-252-991A-7335
; Sequence 7335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7335
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7335

Query Match   12.5%; Score 269.4; DB 4; Length 1737;
Best Local Similarity   50.6%; Pred. No. 9.6e-77;
Matches 823; Conservative   0; Mismatches 776; Indels 28; Gaps   6;

Qy   341 CGCAGAACAAATTAAATTGACACTTTGACAAGCTCAAGGTGTGAAGCGGAATTTAGGTTTGGT 400
         |||||||| |||||||||||||||||||||||||||||||||||
Db   46 CGCCCGAGATCGTCCGTGGGAAACCCCTGGAAGCCCGCGGGTCCCGCCATTGCTACGGCATCGT 105
Qy   401 GGGTTGACAGCAGCCTTAATCCGATCCGGATGCTCGTCCCGGCCAATCAGATATTGAGTGGGTGCA 460
         ||||||| | || |||||||||||||
Db   106 CGGGCGACACCCTCAACCATGTCACCGACGCCATCCATCGCAGCCAGATCCAGTGGGTCCA 165
Qy   461 CGTTCGAAATGAGGAAGGCGCGGCGTTGCAGCCGGTGCGGGAATCGTTGATCACTGGGGA 520
         ||||||| || |||||||||
Db   166 CGTGCGGCCACGAAGAAAGCGGGGCGGCCCTTCGCGCCCGGAGTCCTACATCAGCGGACG 225
Qy   521 GCTGGCCAGTATGTTGCTCGTCCTTCTTGTGTGGTCCTGGGAAAACACACACCTGATTTCAGGGGTCTTTA 580
         |||||| || |||||||
Db   226 CCTGACCGCCTTCGCGCGGGGCTTCCTGCGGACCAGCCCGCCGCCAGCTTCATCAACGGGGTCTA 285
Qy   581 TGATTCCGCATCGAAATGGTTGCGGAAGTGTTGGGCCAGATCGCTAGCCGTATTCCGAGTGCCCA 640
         |||||| |||||||||
Db   286 CGAGGCCCAGCGCAACCGGCGGCCGCCGATGGGTCGCTGATCGGCACGGCCGGGTCCCAGATCGGCA 345
Qy   641 GAATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGACGATTTTGTTTAAGGAAATGCTCTGG 700
         |||||||||
Db   346 ACTGGGGCATGCGAGTTTCCCCAGGAGGTCGACTTCAAGCGGCGTCGCTCTACGGCCAGCTGCGGT 405
Qy   701 TTACTCGGAGATGGTGAAATGGTTGGTGAGCAGGGTGAAACGCATTTTGCATCACGCGGATTCA 760
         |||||||||
Db   406 GTTCTGCGAGCAGCGGTGTCAGCGCCGAACAGGTGGCTGGCCGGCCGATTCCA 465
Qy   761 GTCCACCATGGCGGGTAAAGGTGTGTCCGGTGGTTAGTGATTCCTGGTGATATCGCTAAGGA 820
         ||||||| || |||||
Db   466 GGCGGCGGCTCAACCCGGCGGTTGGCGGTGGTCGATCCGGGCCGGACATC---AGCC 521
Qy   821 AGACCGCAGGTGACGGTACTTATTCCACTATTTCTTCGGCACTCCCGTCGTGTGTT 880
         ||||| | ||
Db   522 AGGCCACGGTGAAGGACGACCTGCGTTCTCGGGTGCATTTCCCGCACCGGGTGCTGCGCC 581
Qy   881 CCCGGGATCCTTACTGAGGCTGCAGCGCCGCGGCGATTAACAACGCTAAGTCTGTGTCAC 940

Qy 1941 CCAACCAATCACGTGGGAAGAACAGTTCATGGGGAATTCAGCAGATCGCAAGAGGGGCCCACCCGAACCGTGTTCTTT 2000
Db
Db 1606 CCGCAGATCAAAACTCGAACACAGCGCCAAAGGTTTCAGCCTGTATATCGTCGCGCAATCATC 1665
Qy
Qy 2001 GGTGGGAGGGAGGTAGGAGGACGGATGATCGGATCTCGGCCCCGGTTCGAAC 2042
Db
Db 1666 AACGGACGCGGGTTGATGAAGTGATCGAACACTGCGGGAAAACAAAC 1707

RESULT 5
US-09-489-039A-4905/c
; Sequence 4905, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4905
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4905

Query Match 10.5%; Score 227.4; DB 4; Length 1293;
Best Local Similarity 52.0%; Pred. No. 3.6e-63;
Matches 641; Conservative 0; Mismatches 571; Indels 21; Gaps 5;

[Nucleotide sequence alignment — Query (Qy) vs Database (Db) rows with connectivity (|) lines]

RESULT 6
US-09-252-991A-7413
; Sequence 7413, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7413
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

Query Match   50.9%; Score 164.2; DB 4; Length 1083;
Best Local Similarity   50.9%; Score 164.2; DB 4; Length 1083;
Matches 469; Conservative 0; Mismatches 443; Indels 9; Gaps 3;

```
Qy    561 GTGGGAGTTCGCAGCCAAAATTAAAGCCCCATCCGTTCCGGCGGGGCAAAGAGACAC 502
Qy   1044 ATCCAGCACATAGAGAATCCGTTTGAGGTCGCGGCATGTCTGGTTGGTTACGGCGGCCTGC 1103
Db    501 GTGGAGTACGACAACCCGTACGAGTGGGCATGACCGGCGGTGATTGGCTTCTCTTCTGGC 442
Qy   1104 GTGGGATGCGTCCAATGAGGCGGGATCTGCTGATTCCATTCCCTTATTCT 1163
Db    441 TTCCACACCATGATGAACCCGATACCCTGATCCTGCTCCAGTTCCCCTATCGC 382
Qy   1164 GATTTCCTTCCTTCCAAAAGAC---AACGTTGCCCAGGTTGCGGCGACATTGGT 1220
Db    381 GCCTTCTACCCACCGACCGGAAAATTATCCAGAATCGGACACTCAAACCCCGGCAGCGGC 341
Qy   1221 CGAGTACCACGGTGAACTGAACTGCGGATATTCCGGTGACGGGTGATGTTGCTGCACAATCGAAAATATT 1280
Db    321 GCACACAGTAAGGTTCGACCATGGCCGCTCGGTGGGCCGATATTAAATCGACACGGCCTG 262
Qy   1281 TTGCCTCATTGTGAAGGAAAAAACAGATACGTTCCTTCCTTGATCGGAATGCTCAAGGCACAC 1340
Db    261 CTGCCCGCTGCTGGAGAGAAAAACGATCGGCCACTTCCTCGAT------AAGGCGCTG 211
Qy   1341 GAGCGTAAGTTGAGCTCGGTGGTTAGAGACGTACACAATAACGTCGGAAGACATGTGCCT 1400
Db    210 GAGCACTATCGGCACGGCCGGAAAAGGGCTCGACGATCTGGCCGGTAAACCCAGCGAATAAAAGCC 151
Qy   1401 ATTCACCCTGAATACGTTGCCTCTTATTTTGAACGAGCTGGGCGGAATGATGCCGTGTTT 1460
Db    150 ATTCACCCGCAAATATCTGGGCGAGACAGTCAGTCATTGTTGCCGATGAAGATGCCATTTTC 91
Qy   1461 ACTGTGGATACCCGGCAATGCAATGTGTGGCAGGGTACATCGGAGGAATCCGGAGGGA 1520
Db     90 ACCTGTGATGTCGGCACCCGACCCGTCTGGGCGGGGGACGCGCTATCTC---AAAATGAATGGT 34
Qy   1521 ACGCGCGGGACTTTGTTGGGTTCAATTCCGCCACGGC 1553
Db     33 AAACGCCGCCTGCTCGGGTCGTTCAACCACGGC 1
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RESULT 7
US-09-252-991A-7281/c
; Sequence 7281, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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Qy    461 CGTTCGAAATGAGGAACGGCGCGCGGTTTGCAGCCGGAATCGTTGATCACTGGGGA 520
Db    162 CGTGCGCCACGAAGAAGCGCGGGCCTTCGCCGGCCGGCGCGGAGTCCTACATCAGCGGACG 221
Qy    521 GCTGGCAGTATGTGCTGCCTTCTTTGTGGTCCTGGAAACACAACCGGAGTCTTTA 580
Db    222 CCTGACCGGCCTTCGCGCGGCCTCCTGCGGGACCGGCGAGCCGCACTTCATCAACGGCGTCTA 281
Qy    581 TGATTCGGCATCGAAATAGTGGCAGAGTGTTGGGCCATCGCTAGCCATTATTCCGAGTCGCCCA 640
Db    282 CGAGGCCGCAGCCGCAACGCGGCGGCCGATAGGTTGCTGATCGGCCAGAGATCGTTACCCCGGCA 341
Qy    641 GATTGGTTCGACGTTCTTCCAGGAAACGCATCCGGAGGAATTTTGTTAAGGAAATGCTCTGG 700
Db    342 ACTGGGCCATTGCAGTTGTCCCAGGAGGTCGACTTCAAGGCGGTCTTACCGCGGCTGCTCGGT 401
Qy    701 TTACTGCCGAGATGGTGAAATGGTGGTGAGCAGGGTGAACGCATTTGCATCACGGCGGATTCA 760
Db    402 GTTCTGCGACGAGGTGCACAGCCCGGAACAGGCGCGGCCGGGCCCGTGCCCTGCCCA 461
Qy    761 GTCCACCATGGCGGGTAAAGGTGTGTCGGTGGGTAGTGATTCCTGGTGATATCGTAAGGA 820
Db    462 GGCGCGGCCTCAACCCGGCGGCGTGGCGGTGGTGATCCTGCGGCGGCGACATC----AGCC 517
Qy    821 AGACCCAGGTGACCGTACTTATTCCAAATTCCACATATTTCTTCTTCGGCGCTCCTGGTGTGTT 880
Db    518 AGGCCCACGGTGAAGGACGACCTGCCGTTCTCCGGTCAATTCCCGGCAACCGGTGCTGCGC 577
Qy    881 CCCGGATCCTTACTGAGGCTGTGCCAGCGGTGGGAGGCGATTAACAAACGGCTAAGTCGTGTCAC 940
Db    578 CCAGGCAGCGCGAACTGCAGGACACTCGCCCCGGCCTGC--TGGCCCACGCCGCAAGAAGAGATCGG 635
Qy    941 TTTGTTCTGCGGGTGGCGGGCGTGGAAGAATGCTCGGCGGCGAGGGTTGTTGGGAGTTGGCGGAGAA 1000
Db    636 CATCTACGCGCGGCTCGCGGCTGCCCAGGCCGCACGACTTCGTCGGTGCCCCTGGCCCGG 695
Qy   1001 GATTAAAATCACCGATCGGGGCCCATCGCGCTGGGTGTTGAAGCGTAAGCATGAGAATCC 1060
Db    696 CCTGAAGGCCGCCCATCGGCCACACGTCGCGGGCCGCCAAGGAACTTCGTCGAGTACGGACAACC 755
Qy   1061 GTTTGAGGTCGGGCGCATGTCTGGGCTGCTTGGTTACGGCGGCCTGCGGTGGATCAGCGGCCAGAATGA 1120
Db    756 CTTCAACATGGGCGCATGACCGGGGATCGGGGATCCCGGGCCGCTTCACACATGATGACCGA 815
Qy   1121 GGGGGGATCTGCTGATTCCATTCGATTCCCCTTATTCCGGCCTTTCCGATTTCCTTCCT---AA 1177
Db    816 GTGCGACACCCTCCTGCTGCTCGGGCGCCGACTTCGCCGCGCAGTTCTATCCGCAGAA 875
Qy   1178 AGACAACGTTGCCCAGGTGGGATATCAACGGTCGCACATTGGTCGACGTACCACGGTGAA 1237
Db    876 GGCCACCCTGATCCAGTTCGACCGCGATAGGCAGTCACCTGGCGCCGGCCACCCCAATCGA 935
Qy   1238 GTATCCGGTGACCGGTGATGT 1258
Db    936 TCTCGGCGGTGGTCGGCGCACGT 956
```

; SEQ ID NO 7281
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7281

Query Match   7.6%;   Score 164.2;   DB 4;   Length 1113;
Best Local Similarity   50.9%;   Pred. No. 1.2e-42;
Matches 469;   Conservative   0;   Mismatches 443;   Indels   9;   Gaps   3;

Qy   341 CGCAGAACAATTAATTGACACTTTGGAAGTTCAAGGTGNTGAAGCGAAATTTATNGGTTTTGGT 400
          ||||| || | ||| | ||| | |||| || | | | | || | |||| || |||||||
Db   1060 CGCCGAGATCGTCGTGGAAACCCTGGAAGCCGGTCCGCATCGGCATCGT 1001

Qy   401 GGGTGACAGCCTTAATCCGATCGTGGGATGCTGTCCGCCAATCAGATAATTGAGTGGGTGCA 460
          ||||| | | | |||| |||||| || | || | || | || || | ||| |||
Db   1000 CGGCGACACCCTCAACCATGTCACCGACCGCATCATCGCAGCCAGATCCAGCCCAGTGGGTCCA 941

Qy   461 CGTTCGAAATGAGGAGNAGCGGCGGCGGTTTGCAGCCGTGGCGGAATCGTTGATCACTGGGGA 520
          || || | ||| || | | ||| | || | ||| | || | | || |||||| || | || |
Db   940 CGTGGCCGCACGAGAAGAGCGGGCCCTTCGCGCTGCGGCGGCCCGAGTCCTACATCAGCGGACG 881

Qy   521 GCTCGGCAGTATNGTNCGTGCTTCTTGTGGGTCCTGGAAAACACACCTGATTCAGGGGTCTTTA 580
          | ||||||||| |||| || | ||| | ||| || || | | || | || || ||| |||
Db   880 CCTGACCGCCTTGCGCCGGCTTCCTCCGGACCGGCAGCCGTGCACTTCATCAAACGGCGTCTA 821

Qy   581 TGATTGCCATCGAAAATGGTNCGGAAGGTTGTGGCCATCGCTAGCCATAATTCCGAGTGCCCA 640
          ||| |||||| || | || | || | | ||| | ||| ||||| | ||| | |||||||
Db   820 CGAGGCCGCACGGACGCCCGATGAGTGGCGACGATCGAGATGCGTGACTTTACCCGGCA 761

Qy   641 GATTGGTTCGACGTTCTTCTTTGTGGGTCCTGGAAAACACACCCGAGAATTTGTTTAAGGAATGCTCTCTG 700
          || ||||| |||||| || ||| || | ||| || | | | || | | |||| | || | |||| |
Db   700 ACTGGGCATCGGAGTTTCCCCAGGAGTCGACTTCAAAGCGCATCTTCAAAGCTGCTTCGGT 701

Qy   701 TTACTGCAGATGGTGAATGGTGGTGAGCAGGAGGGGTGAACCGCATTTTGCATCACGCGGATTCA 760
          |||||||| ||||||| | |||| ||| || | | | ||| | || | | || |||
Db   760 ACTGGGCATGGGATTTCCCCAGGAGTCGACTTCAAAGCGCATCTTCAAAGCTGCTTCGGT 701

Qy   761 GTCCACCATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGA 820
          | | | ||| | | | | || ||| | | ||| | | |||||| ||| |
Db   760 GTTCTGCGAGCAGGTGCACAGCCCGTGTGTGGGCCCTGGCCTGCCA 641

Qy   821 AGACGCAGTGACCGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCCTGTGGTGTT 880
          || |||| |||| | | ||| || || ||| | || ||| | | | | || || |||
Db   640 GGCGGCGCTCAACCGGCGGCTGGGTTGGGCGGTTGATCCTCGCCGACATC---AGCC 585

Qy   881 CCCCGGATCCTACTGAGGCTGCAGGCGATTAACACGCTAAGTCTGTGTCAC 940
          || |||| | ||||| | | |||| |||| | | || || ||| |||||
Db   584 AGGCCACGGTGAAGGACGACCTGCGTTCTCGGGTGCATTTCCCGAACCCGGTGCTGCGCC 525

Qy   941 TTTGGTTCTCGCGTGCGGGTGAAGAAATGCTCGCGCAGGTGTTGGGAGTTGGGCGGAGAA 1000
          || |||| | || | ||| | || || | | | || | | | || | | ||||| |
Db   524 CCACGACCCGCGAACTGCGCGGGACTGCGCCTGC--TGGCCACGGGAACGAGAGAGATCGG 467

Qy   1001 GATTAAAATACCGAATCGGGCGGCATGGGCCTGCTGGGGTGGGTAAGCAGTACACACACACATGAGAATCC 1060
          || ||| | || || ||| || | |||| | ||| | || ||| ||||| | | | |||| || |
Db   466 CATCTACGCCGCGCTTCCGGCTGCCCATCCCAAAGGACTTCGTGACGTTAACAGGAGATGG 407

Qy   1061 GTTTGAGGTCCGGGCAATGGTCTCGGGCATGCAGTGATCGGTCCAATGA 1120
          | ||| | | ||| || | |||| || | || | || || ||||
Db   406 CCTCAAGGCGCCCATCACCTGCGCCAGACTTCGTGAGTACGACAACCC 347

Qy   346 CTTCAAACATGGGGATCTGATTCTATTGGGTAGGGATTTTCCTTATTCTGATTTCCTTCCT---AA 1177
          || ||| | ||| | | | || || || | | || |||| ||| | |||| | | || | ||
Db   286 GTGGGACACCCTCCTGTGCTCCTCGGGGCCGACTTGCCGGGCAGTTCTTATCGGCAGAA 227

Qy   1121 GGGGGGATCGTCGTGATTCTATTGGGTAGGGATTTTCCTTATTCTGATTTCCTTCCT---AA 1177
          | | |||||| || | | || || | || | ||| || | ||||| || |||
Db   1061 GTTTGAGGTCCGGGCAATGGTCTCGGGCATGCAGTGATCGGTCCAATGA 1120

Qy   166 TCTCGGCGTGGTCCGGTGATGT 146
          || ||| || || ||| || |
Db   1238 GTATCCGGTGACCGGTGATGT 1258

Db   1178 AGACAACGTTGCCCAGGTGGGCGACACGGTGGGCCACATTGGGTCGACGTACCACGGTGAA 1237

Db   1121 GGCGGATCGTCTGATTCTATTGGGTAGGGATTTTCCTTATTCTGATTTCCTTCCT---AA 1177

Db   286 GTGGGACACCCTCCTGTGCTCCTCGGGGCCGACTTGCCGGGCAGTTCTTATCGGCAGAA 227

Db   226 GGCCACCCTGATCCAGGTCGACCGGATGGCAGTCACCTGGGCCCCGCCACCCCATCGA 167

Db   1238 GTATCCGGTGACCGGTGATGT 1258

Db   166 TCTCGGCGTGGTCCGGTGATGT 146

RESULT 8
US-10-096-571-7
; Patent No. 6623944
; Sequence 7, Application US/10096571
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
SEQ ID NO 7
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (57)..(577)
; OTHER INFORMATION: Part of the 5' region (poxB1) of the poxB gene
; NAME/KEY: misc_feature
; LOCATION: (578)..(646)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (1)..(1454)
; OTHER INFORMATION: Mutagene DNA
; NAME/KEY: misc_feature
; LOCATION: (647)..(1398)
; OTHER INFORMATION: Part of the 3' region (poxB2) of the poxB gene
; NAME/KEY: misc_feature
; LOCATION: (1399)..(1454)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
US-10-096-571-7

Query Match   7.2%;   Score 155;   DB 4;   Length 1454;
Best Local Similarity   53.7%;   Pred. No. 1.4e-39;
Matches 345;   Conservative   0;   Mismatches 295;   Indels   3;   Gaps   1;

Qy   1399 CTATTCACCCTGAATACGTTGCCTCTTATTTGAACCAGCTGGCGGATAAGGATGCGCGTGT 1458
          || |||||| ||| | |||| | || ||| || | | || || ||| | | || ||
Db   768 CCATTCACCCGCAATATCTCGGCGCAGCAAATTAGTCATTTTGCCCGCGGATGACGCTATTT 827

Qy   1459 TTACTGTGGATACCGGCCATGTGCATGTTGTGGGCATGCGGAGGTACATCGAGAATCCGGAGG 1518
          ||||| | |||| ||| |||||| ||| || || ||| ||| | | | | ||| || |
Db   828 TCACCTGTGACGTTGGTTACCGCCAACGGGTGTGGGCCGCACGTTATCTAAAA---TGAACG 884

Qy   1519 GAACCGCGGCGACTTGTTGGTGGGTTCATTCCCGCCACCGGACGATGGCTAAATGCGTTGCCTCATG 1578
          |||| | |||| | |||| ||||| | | |||| || ||| || |||| || ||||| |||
Db   885 GCAACGGTGCGCTCGGTTGGTTGCGGTTCGTTTAACCACGGTTCGTGGTGCTACGGCCATGCGCCAGG 944

Qy   1579 CGATTGGTGCCAAAGTGTTGATCGAAAACCCCAGGTGATCGGCGATGTGTGGGCGAGGGTG 1638
          || ||||||||| |||| |||| | || | | ||| | ||| | |||| ||| ||| |
Db   945 CGCTGGGTGCCGCCAGCGACAGAGCCGACGTCAGGTGGTCGCCATGGTGGCGATGGCG 1004

Qy   1639 GTTTGGGGCCATGCGTCGTCGGGTGAGCTTCTCGCACGGTTAAGCTGCGACCAACTTCCGCTGAAGG 1698
          | ||| | ||| |||| | || | ||| || ||||| | || | ||| || | | |||| |||
Db   1005 GTTTTAGCATGTTGATGGGGCCGATTCCTCTCAGTATGGCGAGTAGTGAGAAAACTCCAGTGAAAA 1064

Qy   1699 CTGTGGGTGTTAACAAGCAGTTCTTTGGGCATGGGTGAAGTTGGAGAGTTCTCGTTGGGAGAGGAC 1758
          ||| | | |||||| ||||| | | ||| || | ||| ||| || ||| | ||| |||| ||
Db   1065 TTGTCGTTCTTTAACAACAGCGGTCGTGGCGTTGCGGATGGAGATGGGAGATGAGAAGCTGAGGGCT 1124

Qy   1759 AGCCAGAAATTGGTTACTGACCATGAGGAGAGTGAATTTCGCAGAGATTGCGCGGGCGCTGCGG 1818
          || || |||| ||| |||||||| |||||| | ||||| | ||| | | | ||| |||| |
Db   1759 AGCCAGAAATTGGTTACTGACCATGAGGAGAGTGAATTTCGCAGAGATTGCGCGGGCGCTGCGG 1818

RESULT 9
US-10-096-571-8
Sequence 8, Application US/10096571
Patent No. 6623944
GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts th
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Start codon of the delta poxB allele
; NAME/KEY: misc_feature
; LOCATION: (1)..(605)
; OTHER INFORMATION: 5' region of the delta poxB allele
; NAME/KEY: misc_feature
; LOCATION: (606)..(674)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (675)..(1445)
; OTHER INFORMATION: 3' region of the delta poxB allele
; NAME/KEY: misc_feature
; LOCATION: (1446)..(1448)
; OTHER INFORMATION: Stop codon of the delta poxB allele

US-10-096-571-8
Query Match   53.4%; Score 152.8; DB 4; Length 1448;
Best Local Similarity   7.1%; Pred. No. 7.1e-39;
Matches 344; Conservative   0; Mismatches 297; Indels   3; Gaps   1;

Qy   1399 CTATTCACCCTGAATACGTTGCCTCTATTTGAACGAGCTGCGGGATAAGGATGCGGTGT 1458
            ||||| |||||||||||||| |||||||| |||| |||||||||||||||| |||
Db   796 CCATTCACCCGCAAATACTCTGGGCAGCAAATTAGTCATTTTGCCGCCGGATGACGCTTATT 855

Qy   1459 TTACTGTGGATACCGGCATGTGCAAATGTGTGGCATGCCGAGTTACATCGAGAATCCCGGAGG 1518
            || ||||||||| |||||| |||| ||| |||| |||||||||||||| ||||||||
Db   856 TCACCTGTGACGTTGGTACGCCAACGGTTGTGGGCGGCACGTTATCTAAAAA---TGAACG 912

Qy   1519 GAACGCGGCGACTTTGTGGGTTCATTCCGCACGGCACGATGGCTAATGCGGTTGCCTCATG 1578
            || ||||| |||||| ||||| |||| |||| |||| ||||||| |||||||||||
Db   913 GCAAGCGTCGCCGCTGTGTTAGGTTCGTTTAACCACGGTTCGATGGCTAACGCCATGCGCAGG 972

Qy   1579 CGATTGGTGCGCAAAGTGTTGATCGAAAACCGCCAGGTGTCATCGGATCGGATGGGTG 1638
            |||||||| |||||| ||||| ||| ||||||||||| || ||| |||||||| |
Db   1033 CGCTGGCGGTGCGGCAGGCCAGCAGAGCCAGAAGGTCAGGGTGGTCGCCGGGATTGGCG 1032

Qy   1639 TGGCCAATATCCTGGGAACCTGTACTGATCGAATATCGTCACGGAATCCGTGTCGATCC 1698
            || |||| ||| ||||||||||||||| |||||||||||||||| |||||||||||||
Db   1033 GTTTGGGCGATGCTGCTGGGTGACCTTGAGCTTCTGACCGTTAAGCTGCACACCGGATCC 1032

Qy   1699 CTGTGGGTGGTTTAAACAACAGTTCTTTGGGCATGGTGAAGGTTGGGAGAGTCGTTGGAGAC 1758
            |||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||
Db   1093 TTGTCGTTGTTTTAACAACAGCGTGTCGGGGCTTTTGTTGGGCGATGGCGAGATGGAAAGCTGGTGGGCT 1152

Qy   1759 AGCCAGAATTTGGTACTGACCATGAGCAAGTGAATTTCGCAGAGATTGCGGGGCTGCGG 1818
            |||||| ||| ||| |||||||||||||| ||||||||||||||||||||||||||||
Db   1153 ATTTGACGGTACGGCACGGAACTACACGACAAAACTTTGCCGGACCCTGCCGCAACGCTGCGG 1212

Qy   1819 GTATCAAAATCGGTACGCATCACCGATCCGGAAGAAAAGTTCGGCGAGCTAGCTGAGGCAT 1878
            |||||||||||||||||| |||| ||||||||||||| ||||||||||||||||||||
Db   1213 GCATTACGGGGTATTCCCTGTACTGATCGGCAAAGAAAGTTACGCCGAGAGGCAT 1272

Qy   1879 TGGCAATATCCTGGAACCTGTACTGATCGAATATCGTCACGGAATCCGTGTCGATCC 1938
            || |||| ||||||||||||| ||||||| |||||||||| |||||| ||||||
Db   1273 TCTCCATCGACGGGTCCGGTGTTGGTGGATGTGGTGCGCCAAAGAGAGAGTTAGCGATCC 1332

Qy   1939 CACCAACCATCACGTGGGAACAGGTCATCGGATTCAGCAAGGCCGCAACCGGAACCCGTTCT 1998
            ||| ||||||||| |||||||||||||||||||||||| |||| ||||||||||||
Db   1333 CACCCGACGATCAAACTCGAACAGGCCAAAGGTTTCAGCCTTGTATATCGGTGTGCCGCAATCA 1392

Qy   1999 TTGGTGGAGGAGTAGGAGCCGATGATCGACTCGGCCCGTTCGAA 2042
            |||||||||||||||||||||||||||||||||||||||| |||
Db   1393 TCAGCGGACGCGGTGATGAAGTGATCGGACTGGCGAAAACAAAC 1436

(continued)

Qy   1125 ATTTGACTGACGGCCACGGAACTACACGACACAAACTTTGCCGGACGCGTGCG 1184
Qy   1819 GTATCAAAATCGGTACGCATCACCGATCCGGAAGAAAAGTTCGGCGAGCTAGCTGAGGCAT 1878
Db   1185 GCATTACGGGGTATTCCCTGTACTGATCGAATATCGTCACGGAATCCGTGTCGATCC 1244
Qy   1879 TGGCAATATCCTGGAACCTGTACTGATCGAATATCGTCACGGAATCCGTGTCGATCC 1938
Db   1245 TCTCCATCGACGGGTCCGGTGTTGGTGGATGTGGTGCGCCAAAGAGAGAGTTAGCGATCC 1304
Qy   1939 CACCAACCATCACGTGGGAACAGGTCATCGGATTCAGCAAGGCCGCAACCGGAACCCGTTCT 1998
Db   1305 CACCCGACGATCAAACTCGAACAGGCCAAAGGTTTCAGCCTTGTATATCGGTGTGCCGCAATCA 1364
Qy   1999 TTGGTGGAGGAGTAGGAGCCGATGATCGACTCGGCCCGTTCGAA 2041
Db   1365 TCAGCGGACGCGGTGATGAAGTGATCGGACTGGCGAAGGGCGAA 1407

RESULT 10
US-08-956-171E-138
Sequence 138, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439
;
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
    LENGTH: 7900 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 138:
US-08-956-171B-138

Query Match   6.4%; Score 138.8; DB 4; Length 7900;
Best Local Similarity 45.0%; Pred. No. 7.8e-34;
Matches 741; Conservative 0; Mismatches 887; Indels 20; Gaps 5;

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Qy    345 GAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAAATTTANGGTTTGGTGGGT 404
              |||| |||  || | |||| || || ||  |  ||||    | |||| ||||
Db   1589 GAAGCATTAGTTAAAGCATTACAAGCATGGATAATAGATCACTTGTATGGTATTCCAGGA 1648

Qy    405 GACAGCCTTAATCCGATCGTTGGATCTGTCCGCCAATCAGATA------TTGAGTGGGTGC 459
              |||  ||   |||| |||  || |||   ||||||||||           |||| ||
Db   1649 GACTCAAATCGAACGCATAGTCGATAGTTACGTACGTGAGAGATCAATTTAAATTTATC 1708

Qy    460 ACGGTTCGAAATGAGGAAGCGCGGCGCCGGTTTGCAGCCGTGGGAAATCGTTGATCACTGGGG 519
          |||  |    ||  | | ||   |||||| ||| ||| || ||||  | ||  ||| |||||
Db   1709 ATGTTACGTCATGAAGAAGTAGCAAGCTTAGCGGGTCTACACAAAAATTAACTGGGTA 1768

Qy    520 AGCTCGGCAGTAGTGCGTCCTTCTTGTTGGTCCTCGGAAACACACCCTGATTCAGGGTCTTT 579
            | | |    || || |    ||| || | ||||  |||||  | | |  ||||| ||
Db   1769 AAATCGGGTCGTGGCATTAAGTATCGGTCTGTTTTAATTCATTTATTAAATGGTATGT 1828

Qy    580 ATGATTCGCATCGAAAATGGTGCGAAGGGTGTTGGGCCCTGGTTTAATTCATTTATTAAATGTT 639
              | || | |||||| |  |  || | |  ||| |||||  |  ||||| | ||
Db   1829 ATGATGCCAAAATGGATAATGTACGCCAATTAATATATCTGGACATTATTCCGAGTCGCC 1888

Qy    640 AGATTGGGTTCGACGTTCTTCCAGGAGAAAACGCCATCCCGGAGATTTTGTTTAAGGAAATGCTCTG 699
          || |   || | |  | ||  ||||||||||     ||||| ||| | ||  ||| || || |
Db   1889 CACTTGGACGAAAGCATTCCAAGAACAAAATTTACAAAATTAATGTGAAGAGTACAG 1948

Qy    700 GTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTGACTTGCATCACGCGATTC 759
            | | | |  |||| || ||  | ||| |||   ||  | | |||||  || || || ||
Db   1949 TTTATAATCACCAAATTGAAAAAAGGTGACAATGTGTTGAAATCGTTAAGCGAAGCAATTC 2008

Qy    760 AGTCCACCATGGGCGGGGTAAAGGTGTGTCGGTGGTAGTGAATCCTCTGTGATATCGCTAAGG 819
          || || |     ||  || ||| |  | |||| |  |||| |  |  ||||| || ||| |
Db   2009 GTACGGCATATGAACAAAAAGGGTGTAGCTCGTTGTTATTTGTCCTAACGAACTTATTAACTG 2068

Qy    820 AAGACGCGCAGGTGACGGTACTTATTCCAACTTCCACTATTTCTTCTGGCACTCCTGTGGGTGT 879
          || | | |   || | | || ||| |||||  || |   ||  |  || || ||| || ||
Db   2069 AAAA---AATTAAGATACAACGAATAACCAGTAGATACATCAAGACAACTAGTTAT 2125

Qy    880 TCCCGGATCCTACTGAGGCTGCAGGGCCTGGTGGAGGCGATTAACACGCTAAGTCTGTGTCA 939
             || ||||  | || || |  |||  || | || || ||||    | |  ||| | || |
Db   2126 CACCAAAAATAATAAAAGACATCAAACGGGCTTAAACTAATTAATAAAGTAAAAAGCCTG 2185

Qy    940 CTTTGTTCTCGCGGTGCGGCCGTGAAGAAATGCTCGCGCGCAGGGTGTTGGGAGTTGCGCGGAGA 999
             || || ||| | |  |  | | |||  || || |  |  ||||| || || | ||| |
Db   2186 TCATGTTAATTGGTGTTCGGAAACATCGGAAACATCCGAAAGATGGTGAATTTATTGAAA 2245

Qy   1000 AGATTAAATCACCGGATCGGGCATGGGCTGGGTGGTAAGCAGTACATCCAGCTGAGAATC 1059
          ||  | |||  ||| ||  || | | |   |  |  | | || |||  || | |||| |
Db   2246 TGGGCTAAAATTCCTGTCATTCATTACCAGCTAAAACAACTTGCCGGATGATCATC 2305

Qy   1060 CGTTTGAGGTCGGCATGTCTCGGCCTGCCTGCCTGGGATGCGTCCAATG 1119
          ||||  || || |   | ||| | || | | | || || || |||| |
Db   2306 CATATAGTATCGGTAACTTAGGTAAAAATCGGTTACCAAAAACATCTTTATCAAACAATGCAGG 2365

Qy   1120 AGGGGGATCTGCTGATTCTTCATTGGGTACCGGAGTTTCCTTATTCTCGGAGTTCCTTCCTAAAG 1179
          ||  | ||  | |||| |  |  |  |||| || | |  ||  | | || |  | | ||| | |
Db   2366 AAGCCGGATTTATTAATTATCGGTTGGTACAAACTATACCATTAACTTACCTAAGA 2425

Qy   1180 ACAACGTTGCCCAGGTGGATATCACGGTCGGACACATTGGTCGTGAGGTACCACGGTGAAGT 1239
           |   |||  || ||    |   |  |  |  ||| ||  | | || |||| ||| |  ||
Db   2426 AAAATATTAAAGCCATTCAAATTGACA------CAAATCCTAAAAATATCGGACACATCGTT 2479

Qy   1240 ATCCGGTGACCGGTGAGATGTTGCTGCAACAATCGGAAAATATTTTGCCCATCGTGAAGAAA 1299
          | || | ||||| ||| || || |  |||||| ||| ||| |||| || || |||| ||||
Db   2480 TCAATATTAATGGTGTAGGTGGAACATGTTGGAGATAGTAAAATTGCGTTGCATCGTGAGCT 2539

Qy   1300 AAACAGATCGTTCCTTCCTTGATCGGATGCT---CAAGGCACGACGAGCGTTGAGCT 1356
          ||  | |  |  | ||   | |  | |  ||    || | |  | | | ||| || |
Db   2540 ATATTAAAACATGTTGCTGAAAGACCAATTCTTAAACAAAAACGTTAGAACGTAAAGCCGTTT 2599

Qy   1357 CGGTGGTGAGAGTACACACATTAACGTTCGAGAAGAGCATTGCCTATTCACCCTGAATACG 1416
           |  | || |  || | ||| || || |  || | ||||| | | || |||| || | ||
Db   2600 GGGTAAAATGGAATGGAACAGAATAAATAATAATAACATTACGTCCAGAAACGGAT 2659

Qy   1417 TTGCCTCTTATTTTGAACGAGCTGGGCCGGATAAGGATACGGGGTGTTTACTGTGTGATCGTA 1476
          ||||  |  |   | | || || ||  | ||  | | |  ||| | | |   ||  |  | ||
Db   2660 TAATGGCATCAATCAATAAATTATTAAATGATAGTAAGATTGCTCAGCAGATGTTAGGTA 2719

Qy   1477 TGTGCAATGTGTGGCATGCGGAGGTACATCGAGAATCCGGAGGGGAACGCGCGGACTTGTGG 1536
          |||| |||  || |||||  ||| |||||  |||  |  ||||| || | ||| | |||||
Db   2720 CAGCACAGTTTGTTGGCATGTGCCTAAATGGGTCTTGCCTCATGCGATTGGTGCGGAAAGTG 2776

Qy   1537 GTTCATTCCGCCACGGCACGATGGCTAAATGGGTTGCCTCATGCGATTGGTCGGAAAGTG 1596
          |||| || ||| || |  |||| |   ||  |    || || || ||| || ||| | ||
Db   2777 TTTCAAGTTGGTTAGGTTACAATGGGTTGCGGGTCGTTCCAGGTGCAATTGCATCAAAAATTG 2836

Qy   1597 TTGATCGAAACGCCAGGTGTAGCTGACGCACCAACTTCCGGTGGATGGTGGTGTTTGGGTTCGTG 1656
          ||||  |   | |||||||| | ||  | |  | | |  || | | |||  | |  |||| |
Db   2837 CATATCCAAATAGACAAGGCCATCGCAAATTGCTGGTGACGGTGCACTGCCAAGTTCCAGATGAAGTGC 2896

Qy   1657 GTGAGCTTCTGCACGTTAAGCTGACCAACTTCCCGGCTGAAGCTGTTGTTGGGCATGCTGCTGG 1716
          || ||| | ||  | ||| | | |   |||||| ||  || | ||| || |||| | | ||
Db   2897 AAGACTTCGCTACAGCAGCAGTGTAGGCAGCAGTGGTTGTGAATTAGAACAGCAGTTG 2956

Qy   1717 GTTCTTTGGGCATGGTGAGAGTTGGGAGAATGCTCGTCGGTGAGGGACGACGCAGAATTGGGTACTG 1776
           || || ||  |  |  | ||| || | |||  ||  |   ||| | |   | ||||| ||| |||
Db   2957 AAGACTTAGCATTATTATTAAAATATGGAACAAACAAGCAGCTGGTGGATTAGAATATGCAGTG 3016

Qy   1777 ACCATGAGGAAGTGAATTTCGGCAGGAGAATTGCGGCGGTCGGGCCGTTATCGACAAATCGGTACGGCA 1836
          |||| | || | ||| |||| || | || |||  |||  || | | || | | | | |  || | |
Db   3017 ATTTTCTGATATGGAAGCATCTCAAAAATTTGCTCAGCATTTGTTGAGGCGGAGTATAATCCTGAACA 3076

Qy   1837 TCACCGGATCCGAGAGAAAGTTCCGCAGCAGCGTAGCTCGAGGAGCATTAGCAGATGTACCAACCTG 1896
          || |  ||  |||| |  || | |||||||| | ||  ||   || ||| |||| || ||| ||
Db   3077 TTAAGAGTGCTTAGCGGAGTAGAGTCATTAGCTCGAAGAGGGCATTAGCAAGAGATGTACCAA 3136

Qy   1897 TACTGGATCCGGATATCGTCACGGATCCTTAAATGGGGCTGCTGTCGATCCCCAACCATCACGTGGG 1956
          ||| | || || |||  |  |||| || | ||||||  | |||  ||| ||| | | || ||| |
Db   3137 CGATTGGTAGATGTATAATGTTGATCCTCAAATGCTGCGGCCATTACCAGGTAAAAATTGTAAAATG 3196

Qy   1957 AACAGGTTCATGGGATTCAGCAAGGCCGC 1984
          || | |||  |||| || ||||||| | |
Db   3197 AAGAGCGGCTTCGGTTGTTATGGAAGTGGGC 3224
```

RESULT 11
US-08-781-986A-138
; Sequence 138, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
;   APPLICANT: Charles Kunsch
;   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;   NUMBER OF SEQUENCES: 5255
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2

```
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 7900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-138

Query Match      45.0%;  Score 138.8;  DB 4;  Length 7900;
Best Local Similarity   6.4%;  Pred. No. 7.8e-34;
Matches  741;  Conservative 0;  Mismatches 887;  Indels 20;  Gaps 5;
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```
Qy    345  GAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAACCGAATTAATGGTTGGTGGGGT  404
Db   1589  GAAGCATTAGTTAAAGCATTACAAGCACATGGGATATAGACACTTGTATGGTAATTCCAGGA  1648

Qy    405  GACACGCCTTAATCCGATCGTCTGGGATGCTGTCCGGCCAATCAGATA-----TTGAGTGGGTAGC  459
Db   1649  GACTCAAATCCGACGCATAGTCGATAGTTTACGTACAGTGAGAGATCAATTAAATTTTATC  1708

Qy    460  ACGTTCGAAATGAGGAAGCGGGCGCCGGTTTGCAGCCGGTGCGGAATCGTTGAATCGTGGGG  519
Db   1709  ATGTACGTCATGGAAGAAGTAGCAAGCTTAGCGCGCTGCTGGTTACACAAAATTAACTGGTA  1768

Qy    520  AGCTGGCGAGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACCTGATTCAGGGTCTTT  579
Db   1769  AAATCGGTGTGGCATTAAGTATCGGGTGGCCCTGGTTTAATTCATTTAATGGTGTATGT  1828

Qy    580  ATGATTCCGCATCGAAAATGGTGCCGAAGGTGTGTTGGCCATGCCTAGCCATATCCGAGTGCCC  639
Db   1829  ATGATGCAAAANGGGATAAAGTACCCGCAATTAATAATATTCTGGACAAAGATAGTACAG  1888

Qy    640  AGATTGGTTCGCAGCGTTCTTCCAGGAAAACGCATCCCGAGATTTGTTTAAGGAAATGCCTG  699
Db   1889  CACTTGGAACGAAAGCATTCCAAGAGAACAAAATTACAAAANATATGTGAAGAGTAGCCG  1948

Qy    700  GTTACTGCGAGATGGTGAAATGGTCGCGTAGTAGTAGTGTGATGATCGGGTATAATCGCTAAGG  759
Db   1949  TTTATAATCACCAAATTGAAAANGGTGAACGGACATTTGCATCACGCGATTC  2008

Qy    760  AGTCCACCATGGCGGGTGTAAGGTGTGTCGGTGATGANTCCTGGGTAGTGAATCGTTAAGG  819
Db   2009  GTACGGCAGCTGACAGGGTACTGGGTAGTTGTTGTTCCTAACGCACTTATTATCGCTAACTG  2068

Qy    820  AAGAGCGCAGCTGACGGCTACTTATTCCAATTCCACTATTCTTCTGGCACTCCTGTCGGTGT  879
Db   2069  AAAA-----AATTAAAGATACAACAGAATAAACCAGTAGAATACATCAAGACCACAGTAGTAT  2125

Qy    880  TCCCCGGATCCTACTTGAGGCTGCACGCGCTGGTGGAGGCCGGATTAAACACGCTAAGTCTGTCA  939
Db   2126  CACCAAAATATAAAGAGACATCAAAAAAACGGGTTAAACTAATTAATAAAGTAAAAGCCTG  2185

Qy    940  CTTTGTTCTCGCGGTCGCGGCGTGGGTGGTAAGCAGTGTTGGAGTTGGGGGGAGA  999
Db   2186  TCATGTTAATTGGTGTAGGTGCGCAAACATGCCAAACATGAGCTAGTGAATTTATTGAGAG  2245

Qy   1000  AGATTAAATCACCGAATCGGGCACATGCGCGCTGGGTTGGGTCGTACATCCAGCATGAGAATC  1059
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Db   2246  TGGCTAAAATTCCTGTCATTCATTCATTACCAGCTAAAACAAATCTTGCCGGATGGATCATC  2305
Qy   1060  CGTTTGAGGTCGGCATNGTCTCGGCCCTGCTTGGTTACGGCGCCAATGC  1119
Db   2306  CATATAGATACCGGTAACTTAGGTAAAATCGGTTAAAACATCTTATCAAACAATGCAGG  2365
Qy   1120  AGGCGGACTCGCTGATTCTATTGGTATGGTACGGANTTTCCTTATTCTGATTTCCTTCCTAAAG  1179
Db   2366  AAGCGGAGTTATTAAATTATATGGTTGGTACAAAACTATCCATAGTGGATTACTTACCTAAGA  2425
Qy   1180  ACAACGTTGCCCAGGTGCGATATCACACGGGTCGGCACANTTGGTTCGACGGTACCACGGTGAAGT  1239
Db   2426  AAAATATTAACGCCATTCAAAATTGACA------CAAATCCTAAAAATATCGGGACATCGTT  2479
Qy   1240  ATCCGGTGCGACCGGTGANTGTTGCTCGAACAATCGAAAAATAATATTTGGCCTCATGTGAAGGAAA  1299
Db   2480  TCAATATTAATGTAGGAAAATTGTTTGGAGATAAAAATTGCGTTGCATCGAGGATGTTAAACTGAAA  2539
Qy   1300  AAACAGAATCGTTCCTTCCTTGATCGGATGCT----CAAGGCACACGAGCGGTAAGTTGAGCT  1356
Db   2540  ATATTAAACANGTTCCGTGAAAGACCAATTCTTAAACAAAAGTTAGAAGCTAAAAGCGGTTT  2599
Qy   1357  CGGTGGTTAGAGACGTTACACACATAACGTCGAGAAGCANTGTGCCTATTCCACCCTGAANTACG  1416
Db   2600  GGGATAAAATGGATGGAACAAGATTAAAATATAATAATAGTGAAACCATTACGTCCAGAACGAT  2659
Qy   1417  TTGCCTCTATTTTGAACGAGTCGGCGGATAAGGATGCGGTGTTGTTTACTGTNGGATACCGGCA  1476
Db   2660  TAATGGCATCAATCAATAAATTTAATTAAAGATNTGGAGATGAATCCGGTTAGGTTA  2719
Qy   1477  TGTNGCAANTGTGTGGCATGCGGAGGTACANTCGAGAATCGGAGGGAAACGCGCGGACTTTGTGTGG  1536
Db   2720  CAGCAACAGTTTGGTTCGAACTCGATACTT---AAACCTTGGTGTAAATAAACAAGTTCATCA  2776
Qy   1537  GTTCANTCCGCACGCAGCACGATGGGTAAATGCGTTGCCTCANGCGATTGGTGTCGCGAAAGTG  1596
Db   2777  TTTCAAGTNGGTTAGGTTACAAATGGGTTGCGGTCTTCCAGGTTGCATCAAAAATTG  2836
Qy   1597  TTGATCGAAACCGCCAGGTGANTCGCGATGNTGTTGGTNGGGCGATGGTTGGTTTGGGCATGCTGG  1656
Db   2837  CATATCCAAATAGACAAGCCANTCGGCAAATTGCTCTGGTGACCGTGCANTCCANANTGGTAANTGC  2896
Qy   1657  GTGAGCTTCTCGACCCGTTAAGCTGCGCACCACTTCCCGCTGAAGGCGTTGGTGTTGTTTAACACA  1716
Db   2897  AAGACTTCGCTACAGCAGTACAAATATGANTTAACTGTATTCGTATTNGTACTTAAATAAACA  2956
Qy   1717  GTTCTTTGGGCANTGGTGAGTTGGAGAGTCGGTGGAGGGACAGCAGCAGAATTTGGTACTG  1776
Db   2957  AACAGTTAGCANTTATTAANTATGAACAAGCAGCTGGTGGAATTAGGAATATGCAGTTG  3016
Qy   1777  ACCATGAGGAAGTGAGAAAGTTCGGCAGCAGCTAGCTGAGGCANTTGCATTGCCTCTGGACCTG  1836
Db   3017  ANTTTTCTGATATGGATCANTGCAAAAANTTTGCTGAGGCANTTAGAANATGGGTACGGCA  3076
Qy   1837  TCACCGANTCGGAACGAAAAGTTCGGGACAGCAGCTAGCTGAGGCANTTGCATCCTGGACCTG  1896
Db   3077  TTAAGAGTGCTACGGAAGTAGANTGCCANTTAGAGTCGAAGGAGCGCANTTAGCTGTAAAGGTTACCA  3136
Qy   1897  TACTGANTCGAATACGTCACGGANTCCANANTGGCGTTGTCGGANTCCACCANACCANATCACGGTGGGG  1956
Db   3137  CGANTTGTAGGANTGTTATANTGTTGANTCCTANNTGGCGGCANTTACCNANTGTAANTGTAAANTG  3196
Qy   1957  AACAGGTCANTGGANTTCANTGGGCNCANNTGGCGGC  1984
Db   3197  AAGAAGCGCNTTGGTTATNTTGGGCNANTAGTNAGTGGGC  3224
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
;
; SEQ ID NO 7166
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7166

Query Match   6.0%; Score 129.6; DB 4; Length 798;
Best Local Similarity 52.6%; Pred. No.1.7e-31;
Matches 307; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

Qy   1381 ACGTCGGAGGAGCAATGTGCCTATTCACCCTGAATACGGTTGCCTCTTATTTTGAACGAGCTGG 1440
Db   644 AAGCCGGCAAGGGCGAGCTGATCATCCGGTCAGCCTGCTTCGCATCGACCAGCACG 585

Qy   1441 CGGATAAGGATGCGCGGTGTGTTTACTGTGGATACCGGCATGTGCAAATGTGTGGCATGCCGAGGT 1500
Db   584 CCAGCGAGGACGGCCCTGTTCACCGGCGCCGGCCTCGGCGAAGGTCTCGGCTGTTGCGTC 525

Qy   1501 ACATCGAGAATCCGAGGGAAGACGCGCGACTTTGTCGGGTTCATTCCGCACGGCACGGATGG 1560
Db   524 ACATCCACA---GCAACGGCAAGCCGCACCCTCAGGCGGCACCATGG 468

Qy   1561 CTAATGCGTTGCCTCATGCACGGATTGGTCGGCGAAAGTGTTGATCGAAACCGGCCAGGTGATCG 1620
Db   467 CCAACGCCATGCCCACGTGGGCTCGGCGGTCTACCCCGAGCCGCCAGGTGATCT 408

Qy   1621 CGATGTGTGGCGATGGTGGTTTGGGCATGGCATGGCTTCTGACCGTTAAGCTGC 1680
Db   407 CGATCTCCGGCGACCGGCCCTGGCCCATGCTCGGCGGCACTGCTTGACCGGCCATCCAGG 348

Qy   1681 ACCAACTTCCGCTGAAAGGCCTGTGGGTTGTTTAACACAGTTCTTTGGGCCATGGTGAAGTTGG 1740
Db   347 AAAAAACTGCCGATCAAAGGTTAGTGGTGCTGAACAATGCCTCGCTGAACTTCGTCAGCGCTGG 288

Qy   1741 AGATGCTCGTTGGAGGGAAGACAGCCAGAATTTGGTACTGACCATTGAGGAGAGTGAATTTCGCAG 1800
Db   287 AACAGAAGGTTCGAGGGCCTGCTCGGACATGGACTACACCAGAACCCCGGACTTCGCCC 228

Qy   1801 AGATTGCGCGCGGCGTCGCGGTGATATCAAATTCGGTACGCATCACGATCCGGAGAAAGTTCGCG 1860
Db   227 GTCTCGCGCGAGTGAATCGGGCTTCACGGACGCAAGGTGACCGCGCTCCGAGAGCTCGGA 168

Qy   1861 AGCAGCTAGCTGAGGCCATTGGGCAATATCCTGGACCTGTACTGATGATCGGATCGATCTCACGGATC 1920
Db   167 CGGCGGGTTGCGAGGAGTTCCTCGCCCAGCCGCGCCTGCGACGGTGCATACCAACC 108

Qy   1921 CTAATGCGCTGTCGATCCCAACCACCATCACGTGGGGAACAGGTC 1964
Db   107 CTCGCGGGCGTTGGTGATGCCGGCCAGGAGAATCGAGTTCGGCCAGGTC 64

; RESULT 13
; US-09-107-532A-3181
; Sequence 3181, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street

; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinlello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 3181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1746 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1746
; SEQUENCE DESCRIPTION: SEQ ID NO: 3181:
US-09-107-532A-3181

Query Match   5.1%; Score 110.2; DB 4; Length 1746;
Best Local Similarity 44.2%; Pred. No. 5.7e-25;
Matches 653; Conservative 0; Mismatches 803; Indels 21; Gaps 4;

Qy   439 AATCAGATATTGAGTGGGTGCACGTTCGAAATGAGAAGACGCGGCGGCGTTTGCAGCGGTG 498
Db   137 AAACCGGAAATCAACTACATTCAAGTTCGTCATGAAGAAGTCGGCGCACTCGGCAGCCGCTG 196

Qy   499 CGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTTGTTGTGGTTCCTGGGAAACA 558
Db   197 CAGATCGCAAAATTAACGGGGAAAAGTGGGCGCTCGAGGACCTGGGTGCGA 256

Qy   559 CACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTCGGAAGGTGTTGGCCATCG 618
Db   257 CACATTTGATCAAATGGTTTTGTTATGATCGACAGATGGACCATGTCGCCTTAGTTAGCGGTTCT 316

Qy   619 CTAGCCATATTCCGACGTGCCCAGATTGGTTCGGACGTTCTTTCCAGGAAAACGCATCCGAGA 678
Db   317 TAGGACAAGTTGCTTCTCACATCCATGGAACTATAACTCCTTTCCAGGAACTAAATGAAAATC 376

Qy   679 TTTTGTTTAACGGAAATGCTTCGGTTTACTGCGAGATGGTGAATACGGTGGTTGGAGAGGGTGAAC 738
Db   377 CTATTTTCGCAGAGTGTTAGCGTATACAGTCATCAACATGTTGTACAACACACAAAGTTCTTCCGC 436

Qy   739 GCATTTGTCATCACGCGATTCAGTTCCACCATGGCGCGGGTAAAGGTGTGTTGCGTGGTTGGTTAGTTGTGA 798
Db   437 ATGTAGTTAGATTGAAGCCATTAAAGCCGCCCTATGAGCATTAAACGGCGTGGCCTATCGCGTGACTA 496

Qy   799 TTCCTTGGTGATGATCGGTCATAGCAAGAGAGACGCAGGTGACCGGTACTTATTCCAATTCCACTATTT 858
Db   497 TCCCTGTTGATCCTTGGTTTTGTGAGAAATTGACGAACAACTTTTCTCCA---CCGCTCACA 553

RESULT 14
US-09-134-001C-1619
Sequence 1619, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1619
LENGTH: 1761
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1619

Query Match   4.7%;   Score 101.6; DB 3;   Length 1761;
Best Local Similarity 43.6%;   Pred. No. 3.6e-22;   Indels 27;   Gaps 5;
Matches 721; Conservative   0; Mismatches 904;

```
Qy    859 CTTCTGGCACTTCCTGTGGTGTTCCCGGATCCTACTGAGCGCTGAGCGGTGGGAGGCGA 918
              |||  |||      ||||  | |   |||   | || ||  |   |
Db    554 CTCACAAAACAAAGTTGTTGATTATTACCAGAAGAAAAAGATTTTGCTTAGCGCTTTGCCTTATC 613

Qy    919 TTAACAACGCTAAGTTCTGTCACTTTGTTCTGCGGTGCCGGGGAAGAATGCTTTGCCTTATC 978
              |||   |   ||   |  ||||  |||       |||
Db    614 TTGAAAAGCAAAAAACCAGTTCTTTATGTTGGTGGCGGTGCCGGGAAACGGAATTCCGC 673

Qy    979 AGGTGTTGGAGTTGGCGGAGAGGATTAAATCACCGATCCGGATCCGGTGGGTGGGAAGC 1038
               | |  ||  |   |  ||||  |  ||  ||  |  ||| |
Db    674 AAAATCAAAGAATTCTCAGAACATTTTTCAGTTCCTGGTTCCGTTACGAAAAG 733

Qy   1039 AGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATCTTCTGCGCTGTTGGTTACGGGCG 1098
            |  |   |||   |   ||| |      |    |  | |    |   |   |
Db    734 GAATTATTCCTGATGATTATGAAAACTTTCTTGGTTTTGCTGGACGTGCGTCGTTACTAAAC 793

Qy   1099 CCTGCGTGGATGCCGGCGAATCTGCTGATTCTATTTGGGATTACGGATTTTCCCTT 1158
              |||  ||  |    ||  |  |     | ||  |    ||  |  ||
Db    794 CCCGAAAATGAAGCATTGGCAGAAGCCGATCTGAATCTTATTCTGGTTAGCGACTTCCCAT 853

Qy   1159 ------ATTCTGATTCCTTCCTAAAGACAACGTTTGCCCAGTTGGTGATATCAACGGTGCGC 1212
                    |||  | | ||    ||    || |     | ||  |  |  |   |
Db    854 ACATTGATTCTGCATTTTTATCAAACTGCTGAATTTATTTACCCAAATGATCGATTATCGATCGATGT 913

Qy   1213 ACATTGGTTCGACCTTACCACGGTGAAGTATCCGGTTGAGTTGCTGCAACAATCG 1272
            | |||  |||   |    |   ||| | || ||      |    |   |
Db    914 AATTTGACGAGCCCCATGAAAACATCTTTGTTGGATCCTCGGTGATG----CAAACA 964

Qy   1273 AAAATATTTTGCCTCATGTGAAGGAAGAAAAACAGATCGTTTCCTTGATGGATGCTCA 1332
            |||  | |    ||   |  || ||  || |  | || |  |  ||| || |
Db    965 CAGCTTTGCAAGACTTGTTCGAGTTGAGGGATGCCGGCCTGAATGGTAATGTAAGTTGATACCTAG 1024

Qy   1333 AGGCACACGAGGTAGTTGAGCTCGGTGGTAGAGACGTACACATACGTTGAAGAGC 1392
             ||  |  | ||    |   ||  |    || |   |  | |  |    |||  |
Db   1025 CAAATCAAGAAAATAAGAAAAATGGGTAGATCTGATCGGTTTTGAAGATCGAATTTAAATTCTAT 1084

Qy   1393 ATGTGCCTATTCACCCTGAAATACGTTGCTCTTATTTTGAACGAGCTGGTGGCCGGATAAGGATG 1452
            |   |  |    || | || | | |   | | ||   |   || |   ||||||  | |
Db   1085 AAGAACCGATTCGTCCAGAGGCGTGTCTATAAAGAAATCGTATTGTTGGAAGACGAATG 1144

Qy   1453 CGGTGTTTACTGTGGATACGGCAATGTGCATGGCATGGGAGGGTACATCGAGAATC 1512
            |  |||  ||| |  |       |||  |  | |  |  ||   |    |
Db   1145 CGATTTTCGTCACAGATGTCGGTAACGACTATC----CATTCTATTCGTTTATTGAATA 1201

Qy   1513 CGGAGAGGAACGCGCGCCATTTCGTTGGGGTTCATTCCGCACGCGATGGGCTAAGCGGTTGC 1572
            |||   |||     |   ||  ||| || | |  ||  |   || |   | |   |  ||
Db   1202 TACGAAATGGGTAGCATTTPAAGTAATCGGAGGACCTGGTATTGTGCAACATTATTGGTATG 1261

Qy   1573 CTCATCGATTGGTGTGCGGCAAAGTGTTGATCGGACCGTAAGTGTGTGGCG 1632
            |  | |       | ||   | ||  |   | |    |  |||  | |  |
Db   1262 CAGGAGGAATTGCCGCCAACTAAGCTACCCAGAAAAACAATGTTTACCTTAAGTGGTG 1321

Qy   1633 ATGGTGGTTTGGGCATGCGTCGTGGGTAGCTTCTGACACGTTGCACCAACTTCCCG 1692
            |  |||  |  |  |   ||  |   |  |  ||||  |    | | |  ||
Db   1322 GTATATCACCACCAAAATTCAAAAAGGTGATAATGAAGCAAATT 1381

Qy   1693 TGAAGGCTGTGGTGTTTAACAACAGTTCTTTGAGTTGGAAGATGCTCGTGG 1752
            |  | |  ||| | |||| |   |  ||  ||    | | |  |   |
Db   1382 TTATTAAAGTTTGTGTCTTTTCGAATGATATCTTTTCGGTTAATGACGTTATTAACT 1441

Qy   1753 AGGGACAGCGCCAGGAATTTGGTACTACGAGGTGAATGAAGAGAAGGCGCG 1812
            || | |  || |    || |||  ||| | | |   |  | |  |
Db   1442 CGGAACAAAGAAATTGGTGTATTTTAGAGATGACAAAACCAGATTACAACCTAAACAACCAGCT 1501

Qy   1813 CTGCGGGTTATCAAATCGGTACGGCATCACCGATCCGAAGAAAACGTTCTCCGAGCAGCTAGCTG 1872
            |   |  | |  |||  ||  |  ||  |  ||    |  |  |    || |
Db   1502 CGCTCGGGGCAAATAGCTTTACAGTCACGATAGTCCGCAACTTCGATTTGCCTTTGATG 1561

Qy   1873 AGGCATTGGGCATATCCTTGGACCTGTTACTGACTGGATAT 1909
            |  |  |  | |  |||  ||  || || |   ||   ||
Db   1562 CAGCTGCAAAATCAGATCGTCCTGTAGTTAATCGATGGT 1598
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```
Qy    345 GAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTAATGGTTCGGCTGGGGT 404
             | |  | |  | |   ||  | ||  ||  | |  ||  |   ||  |   || |||
Db     43 GAAGCATTAGTTAAGGCAATTACAAACCTGGAATTGTGATCAAATTTATATATGGGTGTTCCTGGC 102

Qy    405 GACAGCCCTTAAATCCGATCGTCTGTGGATGGCGTCCG-----CCAATCAGATATTGAGTGGGTG 458
            || | || || |  | |  || |  |   ||  | ||      ||| |   | ||
Db    103 GACTCAGTAGAAGTCTGTTGTTTCAGAAGCTTACGTTACGGTGTTCAGAGAGATCAATTTAAATTCAT 162

Qy    459 CACGTTCGAAATGAGGAAGACGGCGCGTTTGCGAGCCGGTGCGGAAATCGTTGATCACGTGGG 518
             |  | |   | | ||  || |  |   ||  |    ||| || ||  | ||    |  |||
Db    163 CACGTACGTCATGAACACAGTACGGAGTTTAGCTGCTCGGCAAAATGACACAGGG 222

Qy    519 GAGCTGGCAGTATGTGCTGCTTCCTTGTGTCCTCCTGGGAAACACAGCCACTTGATTCAGGGTCTT 578
             | ||||  | |  |  | |  ||  |  | |   || |   | |   ||  |  ||   | |
Db    223 AAAATTGGTAGCTTPAAGTAATCGGAGGACCTGGTATTGTGCAACATTATTGGTAATGGTATG 282

Qy    579 TATCGATTCGCATCGAAAATGGTGCGAAGGTGTTGGGCATCGGCTAGCGCCATTATTCGGAGTGCC 638
            ||  |||   ||| | ||  | || |  |    |  |||   |    ||| |   |   | ||
Db    283 TACGAAATGGGTAGCATTTAAAGTAATCGGAGGACCTGGTATTGTGCAACATTATTGGTAATGGTACA 342

Qy    639 CAGATTGGTTCGACGTTCTTCCAGGAAAACGCATCCGGAGATTTGGTTTAAGGGAAATGCTCT 698
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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8458
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8458

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; APPLICANT: Marc J. Rubenfield et al.
; GENERAL INFORMATION:
; Patent No. 6551795
; Sequence 8458, Application US/09252991A
US-09-252-991A-8458
RESULT 15

; TITLE OF INVENTION: NUCLIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Maximum Match 100%
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SUMMARIES

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3	2160	100.0	2160	15	US-10-078-167-4	Sequence 4, Appli
4	2160	100.0	2160	15	US-10-336-049-4	Sequence 4, Appli
5	2160	100.0	2160	15	US-10-091-342-4	Sequence 4, Appli
6	2160	100.0	2160	16	US-10-686-736-4	Sequence 4, Appli
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9	2160	100.0	1860	17	US-10-781-014-85	Sequence 85, Appl
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11	944	43.7	944	9	US-10-781-014-89	Sequence 89, Appl
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13	875	40.5	875	15	US-10-143-856-5	Sequence 5, Appli
14	875	40.5	875	15	US-10-078-167-6	Sequence 6, Appli
15	875	40.5	875	15	US-10-336-049-6	Sequence 6, Appli
16	875	40.5	875	15	US-10-091-342-6	Sequence 6, Appli
17	813.8	37.7	875	16	US-10-686-736-6	Sequence 6, Appli
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ALIGNMENTS

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US-09-965-825-1
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Patent No. US2002015099A1
GENERAL INFORMATION:
  APPLICANT: DUSCH, Nicole
  APPLICANT: THOMAS, Hermann
  APPLICANT: THIERBACH, Georg
  TITLE OF INVENTION: CORYNEFORM BACTERIA
  TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID US
  FILE REFERENCE: 21354US0X
  CURRENT APPLICATION NUMBER: US/09/965,825
  CURRENT FILING DATE: 2001-10-01
  PRIOR APPLICATION NUMBER: DE 10048604.5
  PRIOR FILING DATE: 2000-09-30
  PRIOR APPLICATION NUMBER: DE 10117085.8
  PRIOR FILING DATE: 2001-04-06
  NUMBER OF SEQ ID NOS: 14
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Best Local Similarity   100.0%;   Pred. No. 0;
Matches 2160;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    841 ATTCCAATTCCACTATTTCTTCCTGGGATCCTACTCACTGAGGCCTG 900
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Db    841 ATTCCAATTCCACTATTTCTTCCTGGGATCCTACTCACTGAGGCCTG 900

Qy    901 CACCGCTGGGTGGAGGGCGATTAACAACGCTAAGTCTGTCACTTTGGTTCTGCGGTGCGGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCGCTGGGTGGAGGGCGATTAACAACGCTAAGTCTGTCACTTTGGTTCTGCGGTGCGGCG 960

Qy    961 TGAAGAAATGCTCGCGCGCCAGGTGTTGAGTTGGCGGAGAAGATTAAATCACCGGATCGGGGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGAAGAAATGCTCGCGCGCCAGGTGTTGAGTTGGCGGAGAAGATTAAATCACCGGATCGGGGC 1020

Qy   1021 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGGCATGTCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGGCATGTCTG 1080

Qy   1081 GCCTGCTTGGGTTACGGCGGCCGCTGCGTCCAATGAGGCGGAATCTGCTGATTCTAT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCTGCTTGGGTTACGGCGGCCGCTGCGTCCAATGAGGCGGAATCTGCTGATTCTAT 1140

Qy   1141 TGGGTACGGGATTTCCCTTATTCTGATTTCTTCCTAAAGACAACGTTGCCCAGCGGTGGATA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGGGTACGGGATTTCCCTTATTCTGATTTCTTCCTAAAGACAACGTTGCCCAGCGGTGGATA 1200

Qy   1201 TCAACCGTGCCCACAATTGGGTCGACGGTGACCTGAAGTGATCCGGGTGAAGTTGTTG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCAACCGTGCCCACAATTGGGTCGACGGTGACCTGAAGTGATCCGGGTGAAGTTGTTG 1260

Qy   1261 CTGCAACAATCGAAAAATATTTGCCTCATGTGAAGGAAAAACAGATCGTTCCTTG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CTGCAACAATCGAAAAATATTTGCCTCATGTGAAGGAAAAACAGATCGTTCCTTG 1320

Qy   1321 ATCGGATGCTCAAGGCACGACCGTAAGTTGAGCTCGGTAGAGAGCTACACATA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGGATGCTCAAGGCACGACCGTAAGTTGAGCTCGGTAGAGAGCTACACATA 1380

Qy   1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAAATACGTTGCCTCTTATTTGAACGAGCTGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAAATACGTTGCCTCTTATTTGAACGAGCTGG 1440

Qy   1441 CGGATAAGGATGCGGCTGTTACTGTCGAAATCCGGCAAGTGTGTGGTGGCATGCGAGGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGATAAGGATGCGGCTGTTACTGTCGAAATCCGGCAAGTGTGTGGTGGCATGCGAGGT 1500

Qy   1501 ACATCGAGAATCCGGAGGGAAGCGCGCGACTTTGTGGGTTCATTCGG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACATCGAGAATCCGGAGGGAAGCGCGCGACTTTGTGGGTTCATTCGG 1560

Qy   1561 CTAATGCGTTGCCTCATGCGGATTGGTGCGGCCAAAAGTGGTTGATCGGATCGATCG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTAATGCGTTGCCTCATGCGGATTGGTGCGGCCAAAAGTGGTTGATCGGATCGATCG 1620

Qy   1621 CGATGTGTCGGCGATGGTCGGTTGGGCATGCCAGCCGTTCAGCGTTAAGCTGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CGATGTGTCGGCGATGGTCGGTTGGGCATGCCAGCCGTTCAGCGTTAAGCTGC 1680

Qy   1681 ACCAACTTCCGCTGAAGGCTGTGTGGGTGTTTAACAACAGTTCTTCTTGGCAGTTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACCAACTTCCGCTGAAGGCTGTGTGGGTGTTTAACAACAGTTCTTCTTGGCAGTTGGG 1740

Qy   1741 AGATGCTCGTGGAGGGACAGCAGCCAGAATTTCGGCAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATGCTCGTGGAGGGACAGCAGCCAGAATTTCGGCAG 1800

Qy   1801 AGATTGCGGCGGCGCTGCGGGTTATCACGGATCCGGAAGAGGAAGTGGAATGTTCGCG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGATTGCGGCGGCGCTGCGGGTTATCACGGATCCGGAAGAGGAAGTGGAATGTTCGCG 1860

Qy   1861 AGCAGCTTAGCTGGCATTGGGCATATCCTGGACCTGTACTGAATCGATCGTCACGGATC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGCAGCTTAGCTGGCATTGGGCATATCCTGGACCTGTACTGAATCGATCGTCACGGATC 1920

Qy   1921 CTAATGCGGCTGTGCGAGTCCGACCACCAACGCGGGAACAGTCATGGGGCTG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTAATGCGGCTGTGCGAGTCCGACCACCAACGCGGGAACAGTCATGGGGCTG 1980

Qy   1981 CGGCCACCCGGAACCGTCTTTGGTGGAGGAGTGAGCGATGAGATCGGCCCGTTCGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCCGGAACCGTCTTTGGTGGAGGAGTGAGCGATGAGATCGGCCCGTTCGA 2040

Qy   2041 ACATAAGGAATATTCCTACTCCATGATGATTGATACACTTGCTGTTCTCATTGACCGCGA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ACATAAGGAATATTCCTACTCCATGATGATTGATACACTTGCTGTTCTCATTGACCGCGA 2100

Qy   2101 GCGCTTAACTGCCAACATTTCCAGGAATGGGCAGCTCACGCGGTGCCCATGAGATTGCCCT 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2101 GCGCTTAACTGCCAACATTCCAGGATGGGAGCTCACGCGGCCGGTGCCCATGAAGATTGCCCT 2160

RESULT 2

US-10-143-856-3
; Sequence 3, Application US/10143856
; Publication No. US20030109014A1
; GENERAL INFORMATION:
; APPLICANT: BURKE, KEVIN
; APPLICANT: DUNICAN, L.K.
; APPLICANT: McCORMACK, ASHLING
; APPLICANT: STAPLETON, CLIONA
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: Process for the fermentative preparation of
; TITLE OF INVENTION: with amplification of the tkt gene
; FILE REFERENCE: MAS/021123/282432
; CURRENT APPLICATION NUMBER: US/10/143,856
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/986,649
; PRIOR FILING DATE: 17-03-2000
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB
US-10-143-856-3

Query Match   100.0%; Score 2160; DB 15; Length 2160;
Best Local Similarity   100.0%;
Matches 2160; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TTAGAGGCGATTCTCTGAGGTCACTTTTTGTGTGGGGTCGGGGGTCTAAATTTGGCCAGTTTT   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TTAGAGGCGATTCTCTGAGGTCACTTTTTGTGTGGGGTCGGGGGTCTAAATTTGGCCAGTTTT   60

Qy   61 CGAGGCGACCAGACAGGACGTGCCCACGAGAGTGTTTAAATAGGCGGATCGGTGGGCATCTGTGT   120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CGAGGCGACCAGACAGGACGTGCCCACGAGAGTGTTTAAATAGGCGGATCGGTGGGCATCTGTGT   120

Qy   121 TTGGTTTCGACGGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGGAAATCCCAAAAGT   180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTGGTTTCGACGGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGGAAATCCCAAAAGT   180

Qy   181 GGGGCATCCCTGTTTGGTACCGAGTACCCACCCGGGGCCTGAAAACTCCCTGGCCAGGCCGG   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGGCATCCCTGTTTGGTACCGAGTACCCACCCGGGGCCTGAAAACTCCCTGGCCAGGCCGG   240

Qy   241 AAGCGTGGCAACAACTGGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGCGTGGCAACAACTGGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACAC   300

Qy   301 AATAGCCATAAACGTTGAGGGAGTTCAGATGGCACACAGCTACGCAGAACAATTAATTGACA   360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AATAGCCATAAACGTTGAGGGAGTTCAGATGGCACACAGCTACGCAGAACAATTAATTGACA   360

Qy   361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTGGTGGGTGGGTGACAGCCTTAATCCGA   420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTGGTGGGTGGGTGACAGCCTTAATCCGA   420

Qy   421 TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGTGGGTGTGCACGTTCGAAAATGAGGAAGCGG   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCGTGGATGCTGTCCGCCAATCAGATATTGAGTGGTGGGTGTGCACGTTCGAAAATGAGGAAGCGG   480

Qy   481 CGGCGCTTTGCAGCCGCGTGCCGGAATCGTTGATCACTCGGGACTGCCAGTATGTGCTGCTT   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CGGCGCTTTGCAGCCGCGTGCCGGAATCGTTGATCACTCGGGACTGCCAGTATGTGCTGCTT   540

Qy   541 CTTGTGTGGTCCTGGAAACTGAAAACCACAACTGATTCAGGGGTCTTTATGATTCGGCATCGG   600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTTGTGTGGTCCTGGAAACTGAAAACCACAACTGATTCAGGGGTCTTTATGATTCGGCATCGG   600

Qy   601 CGAAGGTGTTGGCCCATGCGTAGCCCATATTCCGAGTGCCCAGATTGGTTCGGACGTTCTTCC   660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGAAGGTGTTGGCCCATGCGTAGCCCATATTCCGAGTGCCCAGATTGGTTCGGACGTTCTTCC   660

Qy   661 AGGAAACGCATCCGGAGATTTGTTTAAGGAAATGCTTCTGGTTACTCGGGAGGATGAATG   720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGAAACGCATCCGGAGATTTGTTTAAGGAAATGCTTCTGGTTACTCGGGAGGATGAATG   720

Qy   721 GTGGTGAGCAGGGTGGAACGCATTTTGCATCACGCGGATTCAGTCCACCATGGGGGGTAAAG   780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTGGTGAGCAGGGTGGAACGCATTTTGCATCACGCGGATTCAGTCCACCATGGGGGGTAAAG   780

Qy   781 GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGACGCGAGGTAGACGGTACTT   840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGACGCGAGGTAGACGGTACTT   840

Qy   841 ATTCCAATTCCACTATTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCACCTACTGAGGCTG   900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATTCCAATTCCACTATTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCACCTACTGAGGCTG   900

Qy   901 CAGCGCTGGGTGGCGGATTAACAAGGCTAAGTCTGTCACTTTGTTCTGTGGTCGGCGGCG   960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGCGCTGGGTGGCGGATTAACAAGGCTAAGTCTGTCACTTTGTTCTGTGGTCGGCGGCG   960

Qy   961 TGAAGAATGCTCGCGCGCGGCCAGCGTTGGGAGTTGGCGGAGAAGATTAAATCACGGATCGGGC   1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGAAGAATGCTCGCGCGCGGCCAGCGTTGGGAGTTGGCGGAGAAGATTAAATCACGGATCGGGC   1020

Qy   1021 ATGGCGTGGGGTGGGTAAGCAGTACATCCAGCATGAGAATCCGGTTTGAGGTCGGCATCTG   1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGGCGTGGGGTGGGTAAGCAGTACATCCAGCATGAGAATCCGGTTTGAGGTCGGCATCTG   1080

Qy   1081 GCCTGCTTGGTTACGGCGCCTGCGGTGGATGGGTCCAATGAGGTCCAAATCTGCTGATTCTAT   1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCTGCTTGGTTACGGCGCCTGCGGTGGATGGGTCCAATGAGGTCCAAATCTGCTGATTCTAT   1140

Qy   1141 TGGGTACGGATTCCCTTAATTCTGATTCTTCCTAAAGACAAGAGGCGGGATA   1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGGGTACGGATTCCCTTAATTCTGATTCTTCCTAAAGACAAGAGGCGGGATA   1200

Qy   1201 TCAAACGGTGCGCACAATTGGTCGACGGTGAAGTCGGTGAAGTATCGGGTTGATGTTG   1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCAAACGGTGCGCACAATTGGTCGACGGTGAAGTCGGTGAAGTATCGGGTTGATGTTG   1260

Qy   1261 CTGCAACAATCGAAAATATTTTGCCCTCATGTGAAGGAAAAACAGATCGTTCCTTCCTTG   1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CTGCAACAATCGAAAATATTTTGCCCTCATGTGAAGGAAAAACAGATCGTTCCTTCCTTG   1320

Qy   1321 ATCGGATGCTCAAGGCACCGAGCGTAAGTGAGTCGGTGAGAGACGTACACATA   1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGGATGCTCAAGGCACCGAGCGTAAGTGAGTCGGTGAGAGACGTACACATA   1380

Qy   1381 ACGTTCGGAAGCGCATGTGCCTATTCACCCTGAATACGTTGCCCTCTATTTTGAACGAGCTGG   1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACGTTCGGAAGCGCATGTGCCTATTCACCCTGAATACGTTGCCCTCTATTTTGAACGAGCTGG   1440

Qy   1441 CGGATAAGGATGGCGCGTGTTTACTGTTGGGTGCATGCAAATGTGTGGCATGGCAGGT   1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGATAAGGATGGCGCGTGTTTACTGTTGGGTGCATGCAAATGTGTGGCATGGCAGGT   1500

Qy   1501 ACATCGAGAATCCGGAGGGAACGCCGGAACACTTTGTCGATACCGGCACGTGTGGCATGG   1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACATCGAGAATCCGGAGGGAACGCCGGAACACTTTGTCGATACCGGCACGTGTGGCATGG   1560

Qy   1561 CTAATCGGTTGCCTCATGCGAACGGATTGGTGCGCAAAGTGTTGATCGAAACCGGCAGGTGATCG   1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTAATCGGTTGCCTCATGCGAACGGATTGGTGCGCAAAGTGTTGATCGAAACCGGCAGGTGATCG   1620

Qy   1621 CGATGTGTGGCGGATGGTGGTTTGGGCATGCTGCTGGGGCATGCTGGACCGGTTAAGCTGC   1680

RESULT 3

US-10-078-167-4

; Sequence 4, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Ciiona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/078,167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB

US-10-078-167-4

Query Match　　　100.0%;　Score 2160;　DB 15;　Length 2160;
Best Local Similarity　100.0%;　Pred. No. 0;
Matches 2160;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Qy        1 TTAGAGGGGATTCTGTGGAGGTCACTTTTTGTGGGGTGCGGGGTCTAAATTCGGCCAGTTT 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TTAGAGGGGATTCTGTGGAGGTCACTTTTTGTGGGGTGCGGGGTCTAAATTCGGCCAGTTT 60

Qy       61 CGAGGCGACCACAGAGCGGGTGCCCACGATGGTTTAAATAGGCGGATCGGTGGGCATCTGTGT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CGAGGCGACCACAGAGCGGGTGCCCACGATGGTTTAAATAGGCGGATCGGTGGGCATCTGTGT 120
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Db       61 CGAGGCGACCACAGAGCGGGTGCCCACGATGTTTAAATAGGCGGGATCGGTGGGCATCTGTGT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      121 TTGGTTTCGACGGGCTGAAAACCAGACTGCCCAGACGGGAAAATCCCAAAAGT 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TTGGTTTCGACGGGCTGAAAACCAGACTGCCCAGACGGGAAAATCCCAAAAGT 180

Qy      181 GGGCACATCCCTGTTTGGTACCGGAGTACCCACCCAGATCGCCGAGGGGCG 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGGCACATCCCTGTTTGGTACCGGAGTACCCACCCAGATCGCCGAGGGGCG 240

Qy      241 AAGCGTGGGCACAACTGGAATTTAAGAGCACAAATTGAAGTCGCACCACGAC 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AAGCGTGGGCACAACTGGAATTTAAGAGCACAAATTGAAGTCGCACCACGAC 300

Qy      301 AATAGCCATAAACGTTTGAGATTTCAGATGGCACACAGCCGAGAACAATTAATTGACA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AATAGCCATAAACGTTTGAGATTTCAGATGGCACACAGCCGAGAACAATTAATTGACA 360

Qy      361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGGTGACAGCCTTAATCCGA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGGTGACAGCCTTAATCCGA 420

Qy      421 TCGTTGGATGCTGTCCCGCCAAATCAGATATTGAGTGGTGGGTGCACGTTCGAAATGACGAAAGCGG 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TCGTTGGATGCTGTCCCGCCAAATCAGATATTGAGTGGTGGGTGCACGTTCGAAATGACGAAAGCGG 480

Qy      481 CGGCGTTTGCAGCCCGTGCGGAATCGTTGATCACTGGGGAGCTGGGCACTAGTGTGGCTGCTT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CGGCGTTTGCAGCCCGTGCGGAATCGTTGATCACTGGGGAGCTGGGCACTAGTGTGGCTGCTT 540

Qy      541 CTTGTGGTCCTGGAAAACACACACCTGATTCAGGGTCTTTATGATTCGATTCGGAAAATGGTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CTTGTGGTCCTGGAAAACACACACCTGATTCAGGGTCTTTATGATTCGATTCGGAAAATGGTG 600

Qy      601 CGAAGGTGTTGGCCATCGGCTAGCCATATTCCGAGTGTGCCCAGATTGGTTCGACGTTCTTCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CGAAGGTGTTGGCCATCGGCTAGCCATATTCCGAGTGTGCCCAGATTGGTTCGACGTTCTTCC 660

Qy      661 AGGAAACGCATCCGGAGGATTTTGTTTAAGGAAATAGCTCTTGGTTACTGCCAGATGGTGAATG 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AGGAAACGCATCCGGAGGATTTTGTTTAAGGAAATAGCTCTTGGTTACTGCCAGATGGTGAATG 720

Qy      721 GTGGTGAGCAGGGTGAACGGCATTTTGCATCACGCGGATTCACGTCCACCATGGCGGGGTAAAG 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GTGGTGAGCAGGGTGAACGGCATTTTGCATCACGCGGATTCACGTCCACCATGGCGGGGTAAAG 780

Qy      781 GTGTGTCGGTGGGTAGTGAATTCCTGGTGATATCGGCTAAGGAAGACGCAGGTGACGGGTACTT 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GTGTGTCGGTGGGTAGTGAATTCCTGGTGATATCGGCTAAGGAAGACGCAGGTGACGGGTACTT 840

Qy      841 ATTCCAATTCCACTATTTCTTCTGGCCACTCCTGTGGTTCCCGGATCCCGGAATCCCTACTGAGGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ATTCCAATTCCACTATTTCTTCTGGCCACTCCTGTGGTTCCCGGATCCCGGAATCCCTACTGAGGCTG 900

Qy      901 CAGCGCTGGGTTGAGAGGCGCATTAAACAGCTAAGTCGTGTCACTTTGTTCTGCGGGTCGGGCG 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CAGCGCTGGGTTGAGAGGCGCATTAAACAGCTAAGTCGTGTCACTTTGTTCTGCGGGTCGGGCG 960

Qy      961 TGAAGAAATGCTTCGGCGCGGCAGGTGTTGGAGTTGGGGGAGAGAATTAAATCACCGGATCGGGC 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TGAAGAAATGCTTCGGCGCGGCAGGTGTTGGAGTTGGGGGAGAGAATTAAATCACCGGATCGGGC 1020

Qy     1021 ATGCGCTGGGTGGGTAAGCAGTACATCGGACATGAGAATCCGTTTGAGGTCGGCANGTCTG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ATGCGCTGGGTGGGTAAGCAGTACATCGGACATGAGAATCCGTTTGAGGTCGGCANGTCTG 1080

Qy     1081 GCCTGCTTGGTTACGGCGCGCCTGCGTGGATGCGGATGGCGGATCTGGATTCTGAGTTCTAT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GCCTGCTTGGTTACGGCGCGCCTGCGTGGATGCGGATGGCGGATCTGGATTCTGAGTTCTAT 1140

Qy     1141 TGGGTACGGATTCCCTTAATTCTGATTTCTTCCTAAAGACAACGGTTGCCCAGTGGGATA 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TGGGTACGGATTCCCTTAATTCTGATTTCTTCCTAAAGACAACGGTTGCCCAGTGGGATA 1200
```

```
Db     1621 CGATGTGTCGGCGATCGGTGGTTTGGGCAATCGTGCTGGGGTGGGAGCTTCTGACGGTTAAGCTGC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1681 ACCAACTTCCGCTGAAAGGCTGGTTGGTGTTTAACAACAGTTCTTTGGGCAATGGGGAAGTTGG 1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 ACCAACTTCCGCTGAAAGGCTGGTTGGTGTTTAACAACAGTTCTTTGGGCAATGGGGAAGTTGG 1740

Qy     1741 AGATCTCGTTCGGGAGGGACAGCCCAGAATTTGGTACTGACCCATGAAGTGAATTCGCAG 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 AGATCTCGTTCGGGAGGGACAGCCCAGAATTTGGTACTGACCCATGAAGTGAATTCGCAG 1800

Qy     1801 AGATTGCGCGGGCTGCCGGGTATCCAAATCGGGTAGCCATCACCGGAAGAAGAAGTTCGCG 1860
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 AGATTGCGCGGGCTGCCGGGTATCCAAATCGGGTAGCCATCACCGGAAGAAGAAGTTCGCG 1860

Qy     1861 AGCAGCTAGCTGAGGGCATTGGCATATCCTGGACCTGTACTGATCGATCGAACCGGATC 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 AGCAGCTAGCTGAGGGCATTGGCATATCCTGGACCTGTACTGATCGATCGAACCGGATC 1920

Qy     1921 CTAATGCGCTGTGATCCCACCAACCATCACGTGGGAACAGGTCATCGTGGGATTCAGCAAGG 1980
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 CTAATGCGCTGTGATCCCACCAACCATCACGTGGGAACAGGTCATCGTGGGATTCAGCAAGG 1980

Qy     1981 CGGCCACCGAACCGTCTTTGGTGGCAGGGAGTAGGAGGCGGATAGGAGGAGGCAGAAGAAAGCGG 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CGGCCACCGAACCGTCTTTGGTGGCAGGGAGTAGGAGGCGGATAGGAGGAGGCAGAAGAAAGCGG 2040

Qy     2041 ACATAAGGAAATATTCCTACTCCATGATGAATTGAATACACTTGTTCATTGACCGCGA 2100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 ACATAAGGAAATATTCCTACTCCATGATGAATTGAATACACTTGTTCATTGACCGCGA 2100

Qy     2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCCGGTGCCCATGAGATTGCCCT 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCCGGTGCCCATGAGATTGCCCT 2160
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RESULT 4
US-10-336-049-4
; Sequence 4, Application US/10336049
; Publication No. US20030175911A1
; GENERAL INFORMATION:
;  APPLICANT: Hans, Stephan
;  APPLICANT: Bathe, Brigitte
;  APPLICANT: Reth, Alexander
;  APPLICANT: Thierbach, Georg
;  APPLICANT: Kreutzer, Caroline
;  APPLICANT: Mockel, Bettina
;  TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification of
;   TITLE OF INVENTION: the zwf Gene
;  FILE REFERENCE: 7601/80158
;  CURRENT APPLICATION NUMBER: US/10/336,049
;  CURRENT FILING DATE:  2003-01-30
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
;  LENGTH: 2160
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (327)..(2063)
;  OTHER INFORMATION: poxB
US-10-336-049-4

  Query Match             100.0%;  Score 2160;  DB 15;  Length 2160;
  Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches 0;  Indels 0;  Gaps 0;
  Matches 2160;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTAGAGGCGATTCGTGAGGGTCACTTTTTGTGGGGTCGGGGTCGGGGTCTAAATTTGGCCCAGTTTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAGAGGCGATTCGTGAGGGTCACTTTTTGTGGGGTCGGGGTCGGGGTCTAAATTTGGCCCAGTTTT 60

Qy         61 CGAGGCGACCAGACAGGCGTGCCCACGAGTGTTAAATAGGCGGATCGGTTGGGGTCATCTGT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGAGGCGACCAGACAGGCGTGCCCACGAGTGTTAAATAGGCGGATCGGTTGGGGTCATCTGT 120

Qy        121 TTGGTTTCGACGGGGCTGAAAACCAAACCAGACTGCCCACGCAACGGAAAATCCCAAAAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGGTTTCGACGGGGCTGAAAACCAAACCAGACTGCCCACGCAACGGAAAATCCCAAAAGT 180

Qy        181 GGGCCATCCCTGTTTTGGTACCCAGTACCCACCCGGGGCCTGAAAACTCCCTGGCGAGGGGCCG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGCCATCCCTGTTTTGGTACCCAGTACCCACCCGGGGCCTGAAAACTCCCTGGCGAGGGGCCG 240

Qy        241 AAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTGCCACCAAAGTTAGGCAACAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTGCCACCAAAGTTAGGCAACAC 300

Qy        301 AATAGCCATAACGTTGAGGGAGTTCAGATGGCACACAGCTACGCAGAACAATTAATTGACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AATAGCCATAACGTTGAGGGAGTTCAGATGGCACACAGCTACGCAGAACAATTAATTGACA 360

Qy        361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTGGTGGGGGTAGTCAAGG 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTGGTGGGGGTAGTCAAGG 420

Qy        421 TCGTGGATGCGTCCCGCCAATCAGATATTGAGTGGTGGTGCACGTTCAGAAATGAGGAAGCGG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCGTGGATGCGTCCCGCCAATCAGATATTGAGTGGTGGTGCACGTTCAGAAATGAGGAAGCGG 480

Qy        481 CGGCGTTTGCAGCCGCGGAATCGTTGATCACTGGGAGGTGCGGAGTCCGTAGTATGTGCTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGGCGTTTGCAGCCGCGGAATCGTTGATCACTGGGAGGTGCGGAGTCCGTAGTATGTGCTT 540

Qy        541 CTTGTGGTTCCTGGAAACACACCTGATTCAGGGGTCTTTATGATTGGCATTGAAATGGTG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGTGGTTCCTGGAAACACACCTGATTCAGGGGTCTTTATGATTGGCATTGAAATGGTG 600

Qy        601 CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATATTCCGAGTGCCCAGATATTCCGAGTCCTTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATATTCCGAGTCCTTCC 660

Qy        661 AGGAAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCGTGGTTACTCCGAGATGGTGAATG 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGAAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCGTGGTTACTCCGAGATGGTGAATG 720
```

(Second column, continuing alignment)

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Qy       1201 TCAACGGTGCGGCACATTGGTGCTGACGTACCACGGTGAAGTATCCGGTGATGTTG 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCAACGGTGCGGCACATTGGTGCTGACGTACCACGGTGAAGTATCCGGTGATGTTG 1260

Qy       1261 CTGCAACAATCGAAATATATTTGCCTCAGTCATGTGAACGGAAAAACAGATCGTTCCTTCCTTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCAACAATCGAAATATATTTGCCTCAGTCATGTGAACGGAAAAACAGATCGTTCCTTCCTTG 1320

Qy       1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTTCGGGGTAGGACGTACACACATA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTTCGGGGTAGGACGTACACACATA 1380

Qy       1381 ACGTTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAATTTGAACGAGCTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACGTTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAATTTGAACGAGCTGG 1440

Qy       1441 CGGATAAGGATGCGCGTGTTACTGTGGATACCGGCCAATGTGTGCATGCGAGGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGGATAAGGATGCGCGTGTTACTGTGGATACCGGCCAATGTGTGCATGCGAGGT 1500

Qy       1501 ACATCGAGGAATCCGGAGGGAACGGCGGCGACTTTGTGCGGTTCATTCCGCCCACGGCACGGATGG 1560
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACATCGAGGAATCCGGAGGGAACGGCGGCGACTTTGTGCGGTTCATTCCGCCCACGGCACGGATGG 1560

Qy       1561 CTAATGCGTTGCCTCATGCCAAAGTGTTGATCGAAACCCGCGCCACGGCGAAATCGGATCG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTAATGCGTTGCCTCATGCCAAAGTGTTGATCGAAACCCGCGCCACGGCGAAATCGGATCG 1620

Qy       1621 CGATGTGTGGCGGATGGTGGTTGGGCATGGTCGGGTGAGCTTCTGACCGTTAAGCTGC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CGATGTGTGGCGGATGGTGGTTGGGCATGGTCGGGTGAGCTTCTGACCGTTAAGCTGC 1680

Qy       1681 ACCAACTTCCGCTGAAAGGCTGTGGTTGTTTAACACAGTTGGGGTTGGGGTTGGGTTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACCAACTTCCGCTGAAAGGCTGTGGTTGTTTAACACAGTTGGGGTTGGGGTTGGGTTG 1740

Qy       1741 AGATGCTCGTGGAGGGACACCGAGAATTGGTACTGAAGGAAGTGAATTTCGGCAG 1800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AGATGCTCGTGGAGGGACACCGAGAATTGGTACTGAAGGAAGTGAATTTCGGCAG 1800

Qy       1801 AGATTGCGGGGCGGGGTATCAAAATGGTACGGATCCGGATCCGGAACAGGTTCGCG 1860
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AGATTGCGGGGCGGGGTATCAAAATGGTACGGATCCGGATCCGGAACAGGTTCGCG 1860

Qy       1861 AGCAGCTAGCTGAGGGCATTGGCATATCCTGGACCGTTACTGATCGTCACGGATC 1920
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AGCAGCTAGCTGAGGGCATTGGCATATCCTGGACCGTTACTGATCGTCACGGATC 1920

Qy       1921 CTAATGCCGTGTCGATCCCACCAACCATCACGTGGGAACAGGTCAGCAAGG 1980
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTAATGCCGTGTCGATCCCACCAACCATCACGTGGGAACAGGTCAGCAAGG 1980

Qy       1981 CGGCCACCCGGAACCGTCTTTTGGTGGAGGAGTAGGAGCGATGATCGATCTGCGCCCGTTCGA 2040
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCCGGAACCGTCTTTTGGTGGAGGAGTAGGAGCGATGATCGATCTGCGCCCGTTCGA 2040

Qy       2041 ACATAAGGAATATATCCTTCCCATGATGATACACACTGGGTGTGGGTGTGCTT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACATAAGGAATATATCCTTCCCATGATGATACACACTGGGTGTGGGTGTGCTT 2100

Qy       2101 GCGCTTAACTGCCAACACATTTCCAGGAATGGCAGCTCACGCCGGGTGCCCATGAGATTGCCCT 2160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGCTTAACTGCCAACACATTTCCAGGAATGGCAGCTCACGCCGGGTGCCCATGAGATTGCCCT 2160
```

RESULT 5
US-10-091-342-4
; Sequence 4, Application US/10091342
; Publication No. US20030199045A1
; GENERAL INFORMATION:
; APPLICANT: Degussa AG
; APPLICANT: National University of Ireland, Galway
; APPLICANT: Forschungszentrum Julich GmbH
; TITLE OF INVENTION: Process for the fermentative Preparation of L-Amino Acids with
; TITLE OF INVENTION: Amplification of the zwf Gene.
; FILE REFERENCE: 990239BT
; CURRENT APPLICATION NUMBER: US/10/091,342
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB
US-10-091-342-4

Query Match   100.0%; Score 2160; DB 15; Length 2160;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[DNA sequence alignment between Query (Qy) and Database (Db), positions 1–2160, with full identity across the aligned region]

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Qy    301  AATAGCCCATAAACGTTGAGGAGTTCAGATGGCCACACAGCTACGCAGGCGCAGAACAATTAATTGACA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AATAGCCCATAAACGTTGAGGAGTTCAGATGGCCACACAGCTACGCAGGCGCAGAACAATTAATTGACA  360

Qy    361  CTTTGGAAGCTCAAGGTGTTGAAGCGGAATTTATATGGTTTTGGTGGTGGTGACAGCCTTAATCCGA    420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CTTTGGAAGCTCAAGGTGTTGAAGCGGAATTTATATGGTTTTGGTGGTGGTGACAGCCTTAATCCGA    420

Qy    421  TCGTTGGATGCTGTTCCGGCCAATCAGATATTGAGTGAGGAAGCCGG    480
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TCGTTGGATGCTGTTCCGGCCAATCAGATATTGAGTGAGGAAGCGG   480
```

... (sequence alignment continues, Qy/Db paired rows with identity bars, positions 481 through 1440 in the left column) ...

```
Qy   1381  ACGTTCGGAGCAAGCATGTGCCTATTCACCCTGAAATACGTTGCCTCTTATTTTGAACGAGCTCGG  1440
```

... (right column, positions 1381 through 2160) ...

```
Db   1381  ACGTTCGGAGCAGCATGTGCCTATTCACCCTGAAATACGTTGCCTCTTATTTTGAACGAGCTCGG  1440
...
Qy   2101  GCGCCTTAACTCGCCAACACATTTCCAACGAGGATGGCCAGCTCACGCCCGGTGCCCATGAGAGTTGCCCT  2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  GCGCCTTAACTCGCCAACACATTTCCAACGAGGATGGCCAGCTCACGCCCGGTGCCCATGAGAGTTGCCCT  2160
```

```
;     TYPE: DNA
;     ORGANISM: Corynebacterium glutamicum
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (327)..(2063)
;     OTHER INFORMATION: poxB
US-10-686-736-4
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Query Match     100.0%;  Score 2160;  DB 16;  Length 2160;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy        1 TTAGAGGCGATTCTGTGAGGTCACTTTTGTGTGGGGGTCGGGGGTCTAAATTTGGCCAGTTTT 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TTAGAGGCGATTCTGTGAGGTCACTTTTGTGTGGGGGTCGGGGGTCTAAATTTGGCCAGTTTT 60

Qy       61 CGAGGCCGACCAGCACAGCGGTGCCCACCGATGTTTAAATAGGCGGATCGGTGGGCATCTGTGT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CGAGGCGGACCAGCACAGCGGTGCCCACCGATGTTTAAATAGGCGGATCGGTGGGCATCTGTGT 120
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(DNA sequence alignment continues)

```
RESULT 7
US-09-965-825-4
Sequence 4, Application US/09965825
Patent No. US20020150999A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Hermann
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID U
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; FILE REFERENCE: 21354USOX
; CURRENT APPLICATION NUMBER: US/09/965,825
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR APPLICATION FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DB 10117085.8
; PRIOR APPLICATION FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 3248
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (802)..(2538)
; OTHER INFORMATION:
US-09-965-825-4

Query Match             100.0%;  Score 2160;  DB 9;  Length 3248;
Best Local Similarity   100.0%;
Matches  2160;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Sequence alignment (Qy = Query, Db = Database):

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Qy      1  TTRAGAGGCGATTCTGTGAGGTCACTTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT    60
Db    476  TTRAGAGGCGATTCTGTGAGGTCACTTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT   535

Qy     61  CGAGGCGACCAGACAGGCGTGCCCACGAGTGTTTAAATAGGCGATCGGGTGGGCATCTGTGT   120
Db    536  CGAGGCGACCAGACAGGCGTGCCCACGAGTGTTTAAATAGGCGATCGGGTGGGCATCTGTGT   595

Qy    121  TTGGTTTCGACGGGCGCTGAAACCAACAACAGAACTGCCCAGCAAATCCCAAAAGT       180
Db    596  TTCGTTTCGACGGGCTGAAACCAACAACAGAACTGCCCAGCAAATCCCAAAAGT       655

Qy    181  GGGCATCCCTGTTTGGTACCGAGTACCCACCGCGGGCCTCGAAACTCCCTGGCAGGGGGGCG   240
Db    656  GGGCATCCCTGTTTGGTACCGAGTACCCACCGCGGGCCTCGAAACTCCCTGGCAGGGGGGCG   715

Qy    241  AAGGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTGCGCACCAGTTAGGCAACAC   300
Db    716  AAGGCGTGGCAACAACTGGAATTTAAGAGCACAATTGAAGTGCGCACCAGTTAGGCAACAC   775

Qy    301  AATAGCCATAACGTTGAGAGTTCAGATGGCACAGCTACGCAGAACAATTAATTGACA       360
Db    776  AATAGCCATAACGTTGAGAGTTCAGATGGCACAGCTACGCAGAACAATTAATTGACA       835

Qy    361  CTTTGGAAGCTCAAGGTGTGAAGCGCAATTTATTGGTTTGGTTGGGTGACAGCCTTAATCCGA   420
Db    836  CTTTGGAAGCTCAAGGTGTGAAGCGCAATTTATTGGTTTGGTTGGGTGACAGCCTTAATCCGA   895

Qy    421  TCGTGGATGCGTCCGCCAATCAGATATTGAGTGGGGTGCACGTTCGCAGATAATGAGGAAGCGG   480
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Db    896  TCGTGGATGCGTCCGCCAATCAGATATTGAGTGGGGTGCACGTTCGCAGATAATGAGGAAGCGG   955

Db    481  CGGGCGTTTGCAGCCGGGTGCGAAATCGTTGTCACTGGGGAGGGTGGGCAGTATGTGGCCTT   540

Db   1076  CGAAGGTGTTGGCCATGGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGAGGTTCTTCC   1135

Qy    601  CGAAGGTGTTGGCCATGGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGAGGTTCTTCC    660

Qy    541  CTTGTTCGTTCCTGGAAAACACACACCTGATTCAGGGTGTCTTTATGATTCGCATCATCGGTG   600

Db   1016  CTTGTTCGTTCCTGGAAAACACACACCTGATTCAGGGTGTCTTTATGATTCGCATCATCGGTG   1075

Qy    661  AGGAAACGCATCCGGAGCATTTGTTTGTTAAGGAAATGCTCTGGTTTACTGGGGAATG     720
Db   1076  AGGAAACGCATCCGGAGCATTTGTTTGTTAAGGAAATGCTCTGGTTTACTGGGGAATG    1135

Qy    721  GTGGGTCGAGCACAGGGTGAACGCAATTTGCATCACGCGATTCAGTCAGTTCAGTTTCGGGGTAAAG   780
Db   1136  GTGGGTCGAGCACAGGGTGAACGCAATTTGCATCACGCGATTCAGTCAGTTCAGTTTCGGGGTAAAG   1195

Qy    781  GTGTGTCGGTGGTAGTGATTCCCTGGTGATATGCTAAGGAAGCAGAGGTGACGGGTACTT    840
Db   1196  GTGTGTCGGTGGTAGTGATTCCCTGGTGATATGCTAAGGAAGCAGAGGTGACGGGTACTT   1255

Qy    841  ATTCCAAATTCCACTATTTCTTCTGGCACTCCTGTGTTCCCGGATCCTCACTGAGGCTG     900
Db   1256  ATTCCAAATTCCACTATTTCTTCTGGCACTCCTGTGTTCCCGGATCCTCACTGAGGCTG    1315

Qy    901  CAGCGGCTGGTGGTCGGAGGGGATTAACAAGGCTAAGTCTGTCACTTTTTGGTTCTGCGGCG    960
Db   1316  CAGCGGCTGGTGGTCGGAGGGGATTAACAAGGCTAAGTCTGTCACTTTTTGGTTCTGCGGCG   1375

Qy    961  TGAAGAAATGCTCGCGCCGCCAGGGTGGTTGGGAGTGGGGCGGAGATGAGAATTCCGGATCGGGC   1020
Db   1376  CAGCGGCTGGTGGGAGGGGATTAACAAGGCTAAGTCTGTCACTTTTTGGTTCTGCGCATGGTCG   1435

Qy   1021  ATGCGCGTGGGGTGGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCCATGTGTCTG   1080
Db   1436  TGAAGAAATGCTCGCGCCGCCAGGGTGGTTGGGAGTGGGGGCGGAGATGAGAAATCCGGATCGGGC   1495
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```
Db   1556  GCCTGCTTGGTTACGGGCGCCTGCGTGGATGTCCAATGAGGCGGAATCGTCGATTCTAT   1615

Qy   1081  GCCTGCTTGGTTACGGGCGCCTGCGTGGATGTCCAATGAGGCGGAATCGTCGATTCTAT   1140

Db   1496  CAGCGCTGGTGGGAGGCGGATTAACAAGGTACATCCGGGTGTGCGCGGTTCG   1555

Qy   1141  TGGGTACGGATTTCCCTTATTCTGATTTCTTCCTAAAGACAAACGGTTGCCCAGGTGGAATA   1200
Db   1616  TGGGTACGGATTTCCCTTATTCTGATTTCTTCCTAAAGACAAACGGTTGCCCAGGTGGAATA   1675

Qy   1201  TCAAACGGTGCCCACAATTGGTCGGACCGTACCACGGGTGAAGTGAGTAGTTGGACCCGTGAGTGTTG   1260
Db   1676  TCAACCGGTGCCCACAATTGGTCGGACCGTACCACGGGTGAAGTGAGTAGTTGGACCCGTGAGTGTTG   1735

Qy   1261  CTGCAACAATCGAAAAATATTTTGCCTCATGTGAAGGGAAAAAAACAGATCGTTCCTTCCTTG   1320
Db   1736  CTGCAACAATCGAAAAATATTTTGCCTCATGTGAAGGGAAAAAAACAGATCGTTCCTTCCTTG   1795

Qy   1321  ATCGGATGCTCAAGCGACACCAGCGTAAGTTGAGCGTAGAGACGTTCACACATA   1380
Db   1796  ATCGGATGCTCAAGCGACACCAGCGTAAGTTGAGCGTAGAGACGTTCACACATA   1855

Qy   1381  ACGTCGAAGAGAAAGCAGCATGTGCCTATTCACCCGTGAATACGTTGCCTCTCTATTTTGAACGGACTGG   1440
Db   1856  AGGTTCGAGAAGCATGTGCCTATTCACCCGTGAATACGTTGCCTCTCTATTTTGAACGGACTGG   1915

Qy   1441  CGGATAAGGATGCGGTGTTTACTGTGGAATACGGGAGGCCATGGCATGGCTGGGCATTGGGAGAGGT   1500
Db   1916  CGGATAAGGATGCGGTGTTTACTGTGGAATACGGGAGGCCATGGCATGGCTGGGCATTGGGAGAGGT   1975

Qy   1501  ACATCCAGAATCCGGAGGGAACGCGGCGACTTTGTGTGGGTTCATTCCCGCCACGGCACGATGG   1560
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RESULT 8
US-09-738-626-1/c
Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match       100.0%;  Score 2160;  DB 9;  Length 3309400;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2160;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db 2778870 TGAAGAATGCTCGCCGCCCAGGTGTGTTGGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGGC 2778811
Qy    1021 ATGGCGCTCGGGTGGTGGTAAGCAGTACAGCATGAGAGCATGAGAATCCGTTGAGGGTGGGCATGTCTG 1080
Db 2777810 ATGGCCTCGGGTGGTGGTAAGCAGTACAGTCACCAGATGAATCCGTTTGAGGGTCGGCATGTCTG 2777751
Qy    1081 GCCTCCTTGGTTACGGCGCGCCTGCGTTGGGATGGGGTCAAATGAGGCGGATCTGCTGATTCTAT 1140
Db 2777750 GCCTTGCTTGGTTACGGCGCGCCTGCGTTGGATNGGCGGCAGATCTGCTGATTCTTAT 2777691
Qy    1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTTAAAGCAACAGTTGCCCAGGTTGGGATA 1200
Db 2777690 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTTAAAGCAACAGTTGCCCAGGTGGGATA 2777631
Qy    1201 TCAACGGTGCGCCACATTGGTTCGACGTACCCACGGGTGAAGTATCCGGTGACCGGTGAGTTG 1260
Db 2777630 TCAACGGTGCGCACATTGGTTCGACGTACCCACGGGTGAAGTATCCGGTGACCGGTGATGTTG 2777571
Qy    1261 CTGCAACAATCGAAAATATTTTGCCTCCATGTGAAGGAGAAAAAACAGATCGTTCCTTCCTTG 1320
Db 2777570 CTGCAACAATCGAAAATATTTTGCCTCCATGTGAAGGAGAAAAAACAGATCGTTCCTTCCTTG 2777511
Qy    1321 ATCCGGATNGCTCAAGGCACACGAGCGTAAGTTGAGCTGAGACTGACGTACACACATA 1380
Db 2777510 ATCGGATNGCTCAAGGCACACGAGCGTAAGTTGAGCTGAGACGTACACACATA 2777451
Qy    1381 ACGTCGAGAAGCAACATGTGCCTTATTCACCCTGAAATACGTTGCCTCTTATTTTGAACGAGCTGG 1440
Db 2777450 ACGTCGAGAAGCATGTGCCTTATTCACCCTGAAATACGTTGCCTCTTATTTTGAACGAGCTGG 2777391
Qy    1441 CGGATAAAGGATGCGGTGTTTTACTGTGGATACCGGACGCAATGTGCAATGTCATGGT 1500
Db 2777390 CGGATAAAGGATGCGGTGTTTTACTGTGGATACCGGACGCAATGTGCAATGCCGAGGT 2777331
Qy    1501 ACATCGGAGAATCCGGAGGGAACGCGCGGACTTTGTCGGGGTTCATTCCGGCCACAGGATGG 1560
Db 2777330 ACATCGGAGAATCCGGAGGGAACGCGCGGACTTTGTCGGGGTTCATTCCGGCCACAGGATGG 2777271
Qy    1561 CTAATGCGTTGCCTCATTGGTGCGGCAAAGTGTTGATCGAAACCGCCAGGTGAGTCG 1620
Db 2777270 CTAATGCGTTGCCTCATTGGTGCGGCAAAGTGTTGATCGAAACCGCCAGGTGAGTCG 2777211
Qy    1621 CGATGTGTGGCGATGGGTGGTTGGGCATGTGCTGCTGGGGTGAGCTTCTGACCGTTAAGCTGC 1680
Db 2777210 CGATGTGTGGCGATGGGTGGTTGGGCATGCTGCTGGGGTGAGCTTCTGACCGTTAAGCTGC 2777151
Qy    1681 ACCAACTTCCGCTGAAGGCTGTGCGTGTTAACACAGTTCTTGGGCATNGGTGAAGTTGG 1740
Db 2777150 ACCAACTTCCGCTGAAGGCTGTGTGGTTTAACACAGTTCTTGGGCATNGGTGAAGTTGG 2777091
Qy    1741 AGATGTCGTGCTGGAGGGACAGCCAGAATTTGGTACTGACCATGAAGGAAGTGAATTTCGCAG 1800
Db 2777090 AGATGTCGTGCTGGAGGGACAGCCAGAATTTGGTACTGACCATGAAGGAAGTGAATTTCGCAG 2777031
Qy    1801 AGATTGCGCGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCGGAGAGAAAGTTCGCG 1860
Db 2777030 AGATTGCGCGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCGGAGAGAAAGTTCGCG 2776971
Qy    1861 AGCAGCTAGCTGAGGCATTGGCCAATATCCTTGGACCTGTACTGATACTCGTCACGGATC 1920
Db 2776910 CTAATGCGGCTGTCGATCCCACCAGGTGGGAATCCCAGCTCAGCGTCAGCAAGG 2776851
Qy    1921 CTAAGCGCTGTCGATCCCAACCATCAGTGATCGATATCGGTCACGGAT 1980
Db 2776850 CGGCCACCCGAACCGTCTTTGGTGGGAGGAGGCGATGATCAGGTCATGGGGATTCAGCAAGG 2776791
Qy    1981 CGGCCACCCGAACCGTCTTTTGGTGGGAGGAGGCGATGATCAGGTCATGGGGATTCAGCAAGG 2040
Db 2776790 ACATAAGGAATAATTCCTACTCCATGATTGATGATGATACACCTGCTGCGTTCTCATTGACCGCGCA 2776731
Qy    2041 ACATAAGGAATAATTCCTACTCCATGATGATGATGATACACCTGCTGCGTTCTCATTGACCGCGCA 2100
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Qy    2101 GGGCTTAACTGCCAACATTTCCAGGATNGGGCAGCTCAGCGCGGTGCCCATGAGATTGCCCT 2160
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db 2776730 GGGCTTAACTGCCAACATTTCCAGGATNGGGCAGCTCAGCGCGGTGCCCATGAGATTGCCCT 2776671
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RESULT 9
US-10-781-014-85
; Sequence 85, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Kroger, Burkhard
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;   TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
;   TITLE OF INVENTION: PRODUCTION
;   FILE REFERENCE: BGI-126CPCN
;   CURRENT APPLICATION NUMBER: US/10/781,014
;   CURRENT FILING DATE: 2004-02-17
;   PRIOR APPLICATION NUMBER: US 09/602,740
;   PRIOR FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: 60/141,031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 60/143,208
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: 60/151,572
;   PRIOR FILING DATE: 1999-08-31
;   PRIOR APPLICATION NUMBER: DE 19931412.8
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931413.6
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931419.5
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931420.9
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931424.1
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931428.4
;   PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 85
;   LENGTH: 1860
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1837)
;   OTHER INFORMATION: RXN00635
US-10-781-014-85

Query Match   86.1%; Score 1860; DB 17; Length 1860;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  227 CTGGCAGGCGGCGGCGAAGCGTGGCCAACACTGGAATTGAAGAGCACAAATTGAAGTCGCACC 286
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CTGGCAGGCGGCGGCGAAGCGTGGCCAACACTGGAATTGAAGAGCACAAATTGAAGTCGCACC 60

Qy  287 AAGTTAGGCAACAACAATAGCCATAACGTTGAGGAGTTCAGATGGCAACAGCTACGCAGA 346
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AAGTTAGGCAACAACAATAGCCATAACGTTGAGGAGTTCAGATGGCAACAGCTACGCAGA 120

Qy  347 ACAATTAATTGACACTTTGGAAGCTCAAGGTGTTGAAGCGAATTTATGTGTTTGGTGGTGA 406
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ACAATTAATTGACACTTTGGAAGCTCAAGGTGTTGAAGCGAATTTATGTGTTTGGTGGTGA 180

Qy  407 CAGCCTTAATCCGATCGTGGATGCTCGTCCGCCAATCAGATATTGAGTGGGTTGCACGTTCG 466
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CAGCCTTAATCCGATCGTGGATGCTCGTCCGCCAATCAGATATTGAGTGGGTTGCACGTTCG 240
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Qy        467 AAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGC 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAATGAGGAAGCGGCGGCGTTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGC 300

Qy        527 AGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTATGTGCTGCTTCTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTC 360

Qy        587 GCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGG 420

Qy        647 TTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCGACGTTCTTCCAGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTG 480

Qy        707 CGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCAC 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGAGATGGTGAATGGTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCAC 540

Qy        767 CATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGC 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATGGCGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGC 600

Qy        827 AGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGA 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGA 660

Qy        887 TCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTT 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCCTACTGAGGCTGCAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTT 720

Qy        947 CTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAA 1006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCGGTGCGGGCGTGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAA 780

Qy       1007 ATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGA 1066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCACCGATCGGGCATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGA 840

Qy       1067 GGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGA 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTCGGCATGTCTGGCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGA 900

Qy       1127 TCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGT 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCTGCTGATTCTATTGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGT 960

Qy       1187 TGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGT 1246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGT 1020

Qy       1247 GACCGGTGATGTTGCTGCAACAATCGAAAATATTTGCCTCATGTGAAGGAAAAAACAGA 1306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACCGGTGATGTTGCTGCAACAATCGAAAATATTTGCCTCATGTGAAGGAAAAAACAGA 1080

Qy       1307 TCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGA 1366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGA 1140

Qy       1367 GACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAT 1426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACGTACACACATAACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTAT 1200

Qy       1427 TTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGT 1486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGT 1260

Qy       1487 GTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCG 1546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCG 1320

Qy       1547 CCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAA 1606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCACGGCACGATGGCTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAA 1380

Qy       1607 CCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCT 1666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCGCCAGGTGATCGCGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCT 1440

Qy       1667 GACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGG 1726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACCGTTAAGCTGCACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGG 1500

Qy       1727 CATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGA 1786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CATGGTGAAGTTGGAGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGA 1560

Qy       1787 AGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCC 1846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGTGAATTTCGCAGAGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCC 1620

Qy       1847 GAAGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGA 1906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAAGAAAGTTCGCGAGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGA 1680

Qy       1907 TATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCAT 1966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATCGTCACGGATCCTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCAT 1740

Qy       1967 GGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGA 2026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGA 1800

Qy       2027 TCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 2086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCTGGCCCGTTCGAACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 1860

RESULT 10
US-09-738-626-2873
; Sequence 2873, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2873
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-2873

  Query Match             80.4%;  Score 1737;  DB 9;  Length 1737;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1737;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    327 ATGGCACACAGCTAGCCAGACAACAATTAATTGACACTTGGAAGCTCAAGGTGTGAAGCGA 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCACACAGCTAGCCAGACAACAATTAATTGACACTTGGAAGCTCAAGGTGTGAAGCGA 60

Qy    387 ATTTATGGTTTGGTGTGGGTGACAGCCTTAATCCGATCGTGTCTGGATGCTTGTCCGGTGT 446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATTTATGGTTTGGTGTGGGTGACAGCCTTAATCCGATCGTGTCCGGCAATCAGAT 120

Qy    447 ATTGAGTGGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGGAATCCGG 506
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATTGAGTGGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGGAATCG 180

Qy    507 TTGATCACTGGGGAGCTGGGCAGTATGTGCTCGTTTCTTGTGTCTTTCCGGAAACACACCTG 566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTGATCACTGGGGAGCTGGGCAGTATGTGCTCGTTTCTTGTGTCCCGGAAACACACCTG 240

Qy    567 ATTCAGGGTGTCTTTAATGATTCGGCATCGAAATGGTTGGCCATCGTCCTAGCCAT 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATTCAGGGTGTCTTTAATGATTCGGCATCGAAATGGTTGGCCATCGTCCATGCCAT 300

Qy    627 ATTCCGAGTGCCCAGATTGGTTCGACGGTTCTTCTTCCAGAAACGACATCCGGACGATTTGTTT 686
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATTCCGAGTGCCCAGATTGGTTCGACGGTTCTTCTTCCAGAAACGACATCCGGACGATTTGTTT 360

Qy    687 AAGGAAATGCTCTCGGTTACTTCGGAGATGGTTGGTGTCGAGGAAACGCACATTTTG 746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AAGGAAATGCTCTCGGTTACTTCGGAGATGGTTGGTGTCGAGGAAACGCACATTTTG 420

Qy    747 CATCACGCGATTCAGTCACCATGGGCGGGGTAAAGGTGTGTCGGGTAGTGAATTCCTGGT 806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATCACGCGATTCAGTCACCATGGGCGGGGTAAAGGTGTGTCGGGTAGTGAATTCCTGGT 480

Qy    807 GATATCGGCTAAGGAGACGCATGGTTCGACGGTGAGTCGGGTGGTGAGGAAACGCTATTTCTTCTGGC 866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GATATCGGCTAAGGAGACGCATGGTTCGACGGTTCTTCCAATTCCACTATTTCTTCTGGC 540

Qy    867 ACTCCTGTGGTGTTCCCGGATCCTACTGTGACGCGTCAGCGGTGAATAACGCACATTTTG 926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACTCCTGTGTGTTCCCGGATCCTACTGTGACGCGTCAGCGGTGAATAACGCACATTTTG 600

Qy    927 GCTAAGTCTGTCACTTGTTCTTGTCGGGTGCGCGCGTGGAAGAATGCTCGCGCGCCAGGTGTTG 986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTAAGTCTGTCACTTGTTCTTGTCGGGTGCGCGCGTGGAAGAATGCTCGCGCGCCAGGTGTTG 660

Qy    987 GAGTTGGGCGGAGAAGATTAAATCACCGATGTGGGCATGCGCGTGGGTGGGTTGAAGCAGTACATC 1046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GAGTTGGGCGGAGAAGATTAAATCACCGATGTGGGCATGCGCGTGGGTGGGTTAAGCAGTACATC 720

Qy   1047 CAGCATGAGAATCCGTTTGAGGTCGGCCANGTCTCGGCGCTTGGTTACGGCGGCCTGCGGTG 1106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGCATGAGAATCCGTTTGAGGTCGGCCANGTCTCGGCGCTTGGTTACGGCGGCCTGCGGTG 780

Qy   1107 GATGGGTCCAAATGAGGCGGGATCTGCTGGTTGATTCTATTGGGTACGGGATTTCCCTTATTCTGAT 1166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GATGGGTCCAAATGAGGCGGGATCTGCTGGTTGATTCTATTGGGTACGGGATTTCCCTTATTCTGAT 840

Qy   1167 TTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAACACGGTGCGCACATTGGTCGACGT 1226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAACACGGTGCGCACATTGGTCGACGT 900

Qy   1227 ACCACGGTGAAGTATCCGGTGACCCGGTGATGTTGCTGCAACAATCGAAAAATATTTTGCCT 1286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACCACGGTGAAGTATCCGGTGACCCGGTGATGTTGCTGCAACAATCGAAAAATATTTTGCCT 960

Qy   1287 CATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGAAGGCACACACGAGCGT 1346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CATGTGAAGGAAGAAAAACAGATCGTTCGTTCCTTGATCGGAATGCTCAAAGGCGGT 1020

Qy   1347 AAGTTGAGCTCGGTCGGTGGTAGAGACGTACACATAACGTCGAGAAGCATGTGCCTATTCAC 1406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAGTTGAGCTCGGTCGGTGGTAGAGACGTTACACATAACGTCGAGAAGCATGTGCCTATTCAC 1080

Qy   1407 CCTGAAATACGTTGCCTCCTCTATTTTGACGAGCTGGGCGGTGGGCGGATAAGGATGCCGTGTGTTT 1466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCTGAAATACGTTGCCTCCTCTATTTTGACGAGCTGGGCGGTGGGCGGATAAGGATGCCGTGTTTACTGTG 1140

Qy   1467 GATACCCGGCATGTGCAANTGTTGTGGGCATGCGACGGTACAATCGGAGAATCCGGGAACCGC 1526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATACCCGGCATGTGCAANTGTTGTGGGCATGCGACGGTACAATCGGAGAATCCGGGAACCGC 1200

Qy   1527 GACTTTGTGGGTTCATTCCGCCACGGCCACGGATGGCTAANGCGTTGCCTTCANTGCCGATTGGT 1586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GACTTTGTGGGTTCATTCCGCCACGGCCACGGATGGCTAATGCGTTGCCTTCANTGCCGATTGGT 1260

Qy   1587 GCGCAAAGTGTTGATCGAAAACCGCCACGGTGATCGCTGCGCGATCGATCGGTTGGTT 1646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCGCAAAGTGTTGATCGAAAACCGCCACGGTGATCGCTGCGCGATGGTGGTTTGGGC 1320

Qy   1647 ATGCTGCTGTGGGTTGAGCTTCTGACCGGTTAAGCTGCACCAACTTCCGCTGAAGGCTTGCGTG 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGCTGCTGTGGGTTGAGCTTCTGACCGGTTAAGCTGCACCAACTTCCGCTGAAGGCTTGTGGTG 1380

Qy   1707 TTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATGCTCGTGGTGGGAGGCAGCCAGAA 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATGCTCGTGGTGGGAGGCAGCCAGAA 1440

Qy   1767 TTTGGTACTGACCATGAGGAGACTGAATTTCGCAGAGATGCGGCGCGCTGCGGTGTATCAAA 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTGGTACTGACCATGAGGAGACTGAATTTCGCAGAGATGCGGCGCGCTGCGGTATCAAA 1500

Qy   1827 TCGGTACGGCATCACCGATCCGAAGAAAGTTCGGCAGCTAGCTGAGGCGCATTGGCATAT 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCGGTACGGCATCACCGATCCGAAGAAAGTTCGGCAGCTAGCTGAGGCGCATTGGCATAT 1560

Qy   1887 CCTGGACCTGTACTGATCGATATCGTCACGGATCCTAANTGCGGTGTGTGATCCCACCAACC 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CCTGGACCTGTACTGATCGATATCGTCACGGATCCTAANTGCGGTGTGTGATCCCAACC 1620

Qy   1947 ATCACGTGGGAACAGTTCATCGGATTCAGCAAGGCGCGCCACCCGGACCGTCTTCTTGGTGGA 2006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ATCACGTGGGAACAGTTCATCGGATTCAGCAAGGCGCGCCACCCGGACCGTCTTTTGGTGGA 1680

Qy   2007 GGAGTAGGAGCGGATGATCGAGCTGGCCCGTTCGGAACATAAGGAAATATTCCTTACTCCA 2063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGAGTAGGAGCGGATGATCGAGCTGGCCCGTTCGGAACATAAGGAAATATTCCTTACTCCA 1737
```

RESULT 11
US-10-781-014-89
; Sequence 89, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: BGI-126CPCN
; CURRENT APPLICATION NUMBER: US/10/781,014
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 09/602,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/143,208
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/151,572
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931412.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08

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;  PRIOR APPLICATION NUMBER: DE 19931419.5
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931420.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931424.1
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931428.4
;  PRIOR FILING DATE: 1999-07-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 784
;  SEQ ID NO 89
;  LENGTH: 944
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(921)
;  OTHER INFORMATION: FRXA00635
US-10-781-014-89

Query Match   43.7%;  Score 944;  DB 17;  Length 944;
Best Local Similarity  100.0%;  Pred. No. 4.9e-295;
Matches 944;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1143  GGTACGGGATTTCCCTTATTCTATGATTTCCTTCCTAAAGACAAGTTGCCCAGGTGGATATC  1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGTACGGGATTTCCCTTATTCTATGATTTCCTTCCTAAAGACAAGTTGCCCAGGTGGATATC    60

Qy   1203  AACGGTGCGCACATTGGTCGACGTACCACGGGTGAAGTATTCCGGTGACCGGTGATGTTGCT  1262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AACGGTGCGCACATTGGTCGACGTACCACGGGTGAAGTATTCCGGTGACCGGTGATGTTGCT   120

Qy   1263  GCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAACAGATCGTTCCTTCCTTGAT    1322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAACAGATCGTTCCTTCCTTGAT     180

Qy   1323  CGGATGCTCAAGGCACACGACGGTAAGTTCGGTGGTAGAGACGTACACATAAC          1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CGGATGCTCAAGGCACACGACGGTAAGTTGAGCTCGGTGGTAGAGACGTACACATAAC      240

Qy   1383  GTCGGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTGAACGAGCTGGCG      1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  GTCGGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCG     300

Qy   1443  GATAAGGATGCGGTGTTTACTGTGGAATACCGGCCATGTGAAATGTGGCCATGCGGAGGTAC  1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GATAAGGATGCGGTGTTTACTGTGGAATACCGGCCATGTGAAATGTGGCCATGCGGAGGTAC   360

Qy   1503  ATCGAGAATCCGGAGGGAACCGGCGCCGACACTTTGTGGGGTTCATTCCGCCACCGACATGGCT  1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ATCGAGAATCCGGAGGGAACCGGCGCCGACACTTTGTGGGGTTCATTCCGCCACCGACATGGCT   420

Qy   1563  AATGGGTTGCCTCATGCGAGTTGATCGCGAAACCGGCCAGGTGATCGCG            1622
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  AATGGGTTGCCTCATGCGAGTTGATCGCGAAACCGGCCAGGTGATCGCG              480

Qy   1623  ATGTGTGGCCATGGTGGTTTTGGGGCATGCTTCGGGGTGAGCGGTTAAGCTGCAC        1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  ATGTGTGGCCATGGTGGTTTTGGGGCATGCTTCGGGGTGAGCGGTTAAGCTGCAC        540

Qy   1683  CAACTTCCCGTGAAGGGCTGTGGTGTTTAACACAGTGCTCTTGACGTTGGAG        1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CAACTTCCCGTGAAGGGCTGTGGTGTTTAACACAGTTCTTGACGTTGGAG          600

Qy   1743  ATCGTCGTGGAGGGAACAGCCAGGAAGTGAATTGGTACATGACTGAACATTTCGCAGAG    1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ATCGTCGTGGAGGGAACAGCCAGGAAGTGAATTGGTACATGACTGAACATTTCGCAGAG     660

Qy   1803  ATTGGCGGGGCTGCGGGTTATCAAAATCGGTACCGATCCGAAGAGAAGTTCGCGCAG      1862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  ATTGGCGGGGCTGCGGGTTATCAAAATCGGTACCGATCCGAAGAGAAGTTCGCGCAG      720

Qy   1863  CAGCTAGCTGAGGCATTGGCATATCCTGGGACCTGACTGACGATCGATATCGTCACGGATCCT  1922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CAGCTAGCTGAGGCATTGGCATATCCTGGGACCTGACTGACGATCGATATCGTCACGGATCCT   780

Db    781  AATGCGCTGTCGATCCCACCAACCATCACGTGGGACCTGTACTGACGATCGTCACGGATCCT   840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1983  GCCACCCGACCCGACCGTCTTTGGTGGAGGAGGAGGCCATGATCGATCGCCGGTTCGGAC   2042

Db    841  GCCACCCGACCCGACCGTCTTTGGTGGAGGAGGAGGCCATGATCGATCGCCGGTTCGGAC   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2043  ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT                 2086

Db    901  ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT                 944
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RESULT 12
US-09-965-825-3

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;  Sequence 3, Application US/09965825
;  Patent No. US20020150999A1
;  GENERAL INFORMATION:
;  APPLICANT: THOMAS, Hermann
;  APPLICANT: DUSCH, Nicole
;  APPLICANT: THIERBACH, Georg
;  TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID US
;  FILE REFERENCE: 2135US0X
;  CURRENT APPLICATION NUMBER: US/09/965,825
;  CURRENT FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: DE 10048604.5
;  PRIOR FILING DATE: 2000-09-30
;  PRIOR APPLICATION NUMBER: DE 10117085.8
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 3
;  LENGTH: 875
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
US-09-965-825-3

Query Match   40.5%;  Score 875;  DB 9;  Length 875;
Best Local Similarity  100.0%;  Pred. No. 1.2e-272;
Matches 875;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    705  TCGGACGATGGTGAATGGTGGTGAGCAGGGTGAGACCGAGCCATTTGCATCACGCGGATTCAGTCC  764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TGGGAGGATGGTGAATGGTGGTGAGCAGAGGTGAAACCGAGCCATTTGCATCACGCGGATTCAGTCC   60

Qy    765  ACCATGCGGGTGTAAAGGTGTGTCGGTGGTGTAGTGTGATATCGGTAAGGAGAGAC       824
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ACCATGGCGGGTAAAGGTGTGTCGGTGGTGTAGTGTGATATCGGTAAGGAGAGAC       120

Qy    825  GCAGGTGACGTACTTATTCCAATTCCACTATATTCTTCTCGGCACTCCCTGTGGGTTTCCCG    884
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GCAGGTGACGTACTTATTCCAATTCCACTATATTCTTCTCGGCACTCCCTGTGGGTTTCCCG     180

Qy    885  GATCCTACTGAGGCTGCAGGCGTGGTGGAGGCGGATTACAACACGCTAGTCTGTCACTTTG    944
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  GATCCTACTGAGGCTGCAGGCGTGGTGGAGGCGGATTACAACACGCTAGTCTGTCACTTTG     240

Qy    945  TTCTCGGGTGCGGGGGTGAAGAAAGTCTCGCGCCGCGGGAGGTGTTGGAGTTGGCGAAGATT  1004
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TTCTCGGGTGCGGGGGTGAAGAAAGTCTCGCGCCGCGGGAGGTGTTGGAGTTGGCGAAGATT   300

Qy   1005  AAATCACCGATCCGGGCATCGGGCATGCCGGGTAGCCAGTAGTACATCCGATGAGAGAATCCGTTT  1064
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AAATCACCGATCCGGGCATCGGGCATGCCGGGTAGCCAGTAGTACATCCGATGAGAGAATCCGTTT   360

Qy   1065  GAGGTCGGCATGTCTGGCCTGCTTGGTTTACGGCGGCGCCTGCGTGGATGGCGTCCAATGAGGCG   1124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GAGGTCGGCATGTCTGGCCTGCTTGGTTTACGGCGGCGCCTGCGTGGATGGCGTCCAATGAGGCG    420
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Left column

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Qy   1125  GATCTGCTGATTCTATTGGGTACGGGATTCCCTTATTCTGATTCTTGA...AAGACAC  1184
Db   421   GATCTGCTGATTCTATTGGGTACGGGATTCCCTTATTCTGATTCTTGA...AAGACAC  480
Qy   1185  GTTGCCCAGGTGGGATATCAACGGTGGCCACATTGGT...GAAGTATCCG  1244
Db   481   GTTGCCCAGGTGGGATATCAACGGTGGCCACATTGGT...GAAGTATCCG  540
Qy   1245  GTGACCGGTGATGTTGCTGCAACAATCGAAAAATATT...GGAAAAACA  1304
Db   541   GTGACCGGTGATGTTGCTGCAACAATCGAAAAATATT...GGAAAAACA  600
Qy   1305  GATCGTTCCTTCCTTGATCGGATTCAAGGCACACGAG...GGTCGGTGGGTA  1364
Db   601   GATCGTTCCTTCCTTGATCGGATTCAAGGCACACGAG...GGTCGGTGGGTA  660
Qy   1365  GAGACGTACACATAAACGTCGAGAAGCATGTGCCTAT...CGTTGCCTCT  1424
Db   661   GAGACGTACACATAAACGTCGAGAAGCATGTGCCTAT...CGTTGCCTCT  720
Qy   1425  ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTA...GTGCAAT  1484
Db   721   ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTTA...GTGCAAT  780
Qy   1485  GTGTGGCCATGCGAGGTACATCGAGAATCCGGAC...GGTTCATTC  1544
Db   781   GTGTGGCCATGCGAGGTACATCGAGAATCCGGAC...GGTTCATTC  840
Qy   1545  CGCCACGGCACGGATGGCTAATGCGTTGCCTCATGC  1579
Db   841   CGCCACGGCACGGATGGCTAATGCGTTGCCTCATGC  875
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RESULT 13

US-10-143-856-5

; Sequence 5, Application US/10143856
; Publication No. US20030109014A1
; GENERAL INFORMATION:
; APPLICANT: BURKE, KEVIN
; APPLICANT: DUNICAN, L.K.
; APPLICANT: McCORMACK, ASHLING
; APPLICANT: STAPLETON, CLIONA
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: Process for the fermentative preparation of
; TITLE OF INVENTION: with amplification of the tkt gene
; FILE REFERENCE: MAS/021123/282432
; CURRENT APPLICATION NUMBER: US/10/143,856
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/986,649
; PRIOR FILING DATE: 17-03-2000
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-143-856-5

Query Match   40.5%;   Score 875;   DB 15;   Length 875;
Best Local Similarity   100.0%;   Pred. No. 1.2e-272;
Matches   875;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy   705  TGCGAGATGGTGAATGGTGGTGAGCAGGTGAACGGCATTTTGCATCACCGATTCAGTCC  764
Db   1    TGCGAGATGGTGAATGGTGGTGAGCAGGTGAACGGCATTTTGCATCACCGATTCAGTCC  60
Qy   765  ACCATGGCGCGGTAAGGTGTGTCGGTGGTAGTGAGTG...GGAAGAC  824
Db   61   ACCATGGGCGGTAAAGGTGTGTCGGTGGTAGTGAGTG...GGAAGAC  120
Qy   825  GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG  884
```

Right column

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Db   121   GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG  180
Qy   885   GATCTTACTCAGAGGCTGCAGCGCCTGGGTGGAGGC...AAGCTGTCACTTG  944
Db   181   GATCCTACTGAGGGCTGCAGCGCCTGGGTGGAGGC...TCTCACTTG  240
Qy   945   TTCTGCGGTGCGGGCGTGAAGAATGCTCGGCGGCCA...GGAGAGATT  1004
Db   241   TTCTGCGGTGCGGGCGTGAAGAATGCTCGGCGGCCA...GGAGAGATT  300
Qy   1005  AAATCACCGATCGGGCGTGCGCTGGGTGGTAAGGCA...AATCCGTTT  1064
Db   301   AAATCACCGATCGGGCGTGCGCTGGGTGGTAAGGCA...AATCCGTTT  360
Qy   1065  GAGGTCGGCCATGTCTCGGCCCTCCTTGGTTACGGG...GAATCGGCGG  1124
Db   361   GAGGTCGGCCATGTCTCGGCCCTCCTTGGTTACGGG...GAATCGGCGG  420
Qy   1125  GATCTGCTGATTCTATTGGGTACGGGATTCCCTTAT...AAGACAAC  1184
Db   421   GATCTGCTGATTCTATTGGGTACGGGATTCCCTTAT...AAGACAAC  480
Qy   1185  GTTGCCCAGGTGGGATATCAACGGTGGCCACATTGG...GTATCCG  1244
Db   481   GTTGCCCAGGTGGGATATCAACGGTGGCCACATTGG...GTATCCG  540
Qy   1245  GTGACCGGTGATGTTGCTGCAACAATCGAAAAATAT...GGAAAAACA  1304
Db   541   GTGACCGGTGATGTTGCTGCAACAATCGAAAAATAT...GGAAAAACA  600
Qy   1305  GATCGTTCCTTCCTTGATCGGATTCAAGGCACACGA...GGTCGGTGGGTA  1364
Db   601   GATCGTTCCTTCCTTGATCGGATTCAAGGCACACGA...GGTCGGTGGGTA  660
Qy   1365  GAGACGTACACATAAACGTCGAGAAGCATGTGCCTA...CGTTGCCTCT  1424
Db   661   GAGACGTACACATAAACGTCGAGAAGCATGTGCCTA...CGTTGCCTCT  720
Qy   1425  ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTT...GTGCAAT  1484
Db   721   ATTTTGAACGAGCTGGCGGATAAGGATGCGGTGTTT...GTGCAAT  780
Qy   1485  GTGTGGCCATGCGAGGTACATCGAGAATCCGGAC...GGTTCATTC  1544
Db   781   GTGTGGCCATGCGAGGTACATCGAGAATCCGGAC...GGTTCATTC  840
Qy   1545  CGCCACGGCACGGATGGCTAATGCGTTGCCTCATGC  1579
Db   841   CGCCACGGCACGGATGGCTAATGCGTTGCCTCATGC  875
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RESULT 14

US-10-078-167-6

; Sequence 6, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/078,167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-078-167-6

; APPLICANT: Reth, Alexander
; APPLICANT: Thierbach, Georg
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification o
; TITLE OF INVENTION: the zwf Gene
; FILE REFERENCE: 7601/80158
; CURRENT APPLICATION NUMBER: US/10/336,049
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-336-049-6

Query Match   40.5%; Score 875; DB 15; Length 875;
Best Local Similarity 100.0%; Pred. No. 1.2e-272;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   705 TGCGAGATGGTGAATGGTGGTGAGCACGGTGAACGGCATTTTGCATCACGCGGATTCAGTCC 764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TGCGAGATGGTGAATGGTGGTGAGCACGGTGAACGGCATTTTGCATCACGCGGATTCAGTCC 60

Qy   765 ACCATGGCGGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACCATGGCGGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 120

Qy   825 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTCTGGCACTCCCTGTGGTGTTCCCG 884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTCTGGCACTCCCTGTGGTGTTCCCG 180

Qy   885 GATCCTTACTGAGGCTCGAGCGCGTGGGCGGATTAACAACGCTAAGTCTGTTCACTTTG 944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATCCTTACTGAGGCTCGAGCGCGTGGGCGGATTAACAACGCTAAGTCTGTTCACTTTG 240

Qy   945 TTCTGCGGTGCGGTGCGGGCGGGCGTGAAGAATGTCGCGCGCGCAGGTGTTGGGGGACGAAGATT 1004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTCTGCGGTGCGGTGCGGGCGGGCGTGAAGAATGTCGCGCGCGCAGGTGTTGGGGGACGAAGATT 300

Qy   1005 AAATCACCGATCGGGCATCGGGCGCTGGGTGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAATCACCGATCGGGCATCGGGCGCTGGGTGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 360

Qy   1065 GAGGTCGGCATGTCTGGGCGTTGGTTACGGCGCCCTCGGGTGGATGCGTCCAATGAGGCG 1124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGTCGGCATGTCTGGGCGTTGGTTACGGCGCCCTCGGGTGGATGCGTCCAATGAGGCG 420

Qy   1125 GATCTCGCTGATTCTATTCCTTATTCTGAATTCCTGGGTACGGTACCGGATTCGGAATACGGCG 1184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATCTCGCTGATTCTATTCCTTATTCTGAATTCCTGGGTACGGTACCGGATTCGGAATACGGCG 480

Qy   1185 GTTGCCCAGGTGATGTTGCTGCACAAATCGAAAATATTTGCCCATCAGTGAAGGAAAAAACA 1244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTTGCCCAGGTGATGTTGCTGCACAAATCGAAAATATTTGCCCATCAGTGAAGGAAAAAACA 540

Qy   1245 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAGATT 1304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAGATT 600

Qy   1305 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACAGCAGGCTAAGTTGAGCTCGGTGGTA 1364
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACAGCAGGCTAAGTTGAGCTCGGTGGTA 660

Qy   1365 GAGACGTACACAATAACGTCGAGAGCACATGTGCCTATTCACCCTGAAATACGTTGCCTCT 1424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GAGACGTACACAATAACGTCGAGAGCACATGTGCCTATTCACCCTGAAATACGTTGCCTCT 720

Qy   1425 ATTTTGAACGAGCTGGCGGGATAAGGATGCGGTGTTTACGTGTGGATACCGGCCATGTGCAAT 1484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTTTGAACGAGCTGGCGGGATAAGGATGCGGTGTTTACGTGTGGATACCGGCCATGTGCAAT 780

RESULT 15
US-10-336-049-6
; Sequence 6, Application US/10336049
; Publication No. US20030175911A1
; GENERAL INFORMATION:
; APPLICANT: Hans, Stephan
; APPLICANT: Bathe, Brigitte

Query Match   40.5%; Score 875; DB 15; Length 875;
Best Local Similarity 100.0%; Pred. No. 1.2e-272;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   705 TGCGAGATGGTGAATGGTGGTGAGCACGGTGAACGGCATTTTGCATCACGCGGATTCAGTCC 764
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Qy   765 ACCATGGCGGGGTAAAGGTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGAC 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   825 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTCTGGCACTCCCTGTGGTGTTCCCG 884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTCTGGCACTCCCTGTGGTGTTCCCG 180

Qy   885 GATCCTTACTGAGGCTCGAGCGCGTGGGCGGATTAACAACGCTAAGTCTGTTCACTTTG 944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATCCTTACTGAGGCTCGAGCGCGTGGGCGGATTAACAACGCTAAGTCTGTTCACTTTG 240

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1005 AAATCACCGATCGGGCATCGGGCGCTGGGTGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1064
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAATCACCGATCGGGCATCGGGCGCTGGGTGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 360

Qy   1065 GAGGTCGGCATGTCTGGGCGTTGGTTACGGCGCCCTCGGGTGGATGCGTCCAATGAGGCG 1124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGTCGGCATGTCTGGGCGTTGGTTACGGCGCCCTCGGGTGGATGCGTCCAATGAGGCG 420

Qy   1125 GATCTCGCTGATTCTATTCCTTATTCTGAATTCCTGGGTACGGTACCGGATTCGGAATACGGCG 1184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATCTCGCTGATTCTATTCCTTATTCTGAATTCCTGGGTACGGTACCGGATTCGGAATACGGCG 480

Qy   1185 GTTGCCCAGGTGATGTTGCTGCACAAATCGAAAATATTTGCCCATCAGTGAAGGAAAAAACA 1244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTTGCCCAGGTGATGTTGCTGCACAAATCGAAAATATTTGCCCATCAGTGAAGGAAAAAACA 540

Qy   1245 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAGATT 1304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAGATT 600

Qy   1305 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACAGCAGGCTAAGTTGAGCTCGGTGGTA 1364
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Db   601 GATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACAGCAGGCTAAGTTGAGCTCGGTGGTA 660

Qy   1365 GAGACGTACACAATAACGTCGAGAGCACATGTGCCTATTCACCCTGAAATACGTTGCCTCT 1424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GAGACGTACACAATAACGTCGAGAGCACATGTGCCTATTCACCCTGAAATACGTTGCCTCT 720

Qy   1425 ATTTTGAACGAGCTGGCGGGATAAGGATGCGGTGTTTACGTGTGGATACCGGCCATGTGCAAT 1484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATTTTGAACGAGCTGGCGGGATAAGGATGCGGTGTTTACGTGTGGATACCGGCCATGTGCAAT 780

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Qy   1485 GTGTGGCCATGCGAGGTACATCGAGAATCCGGAGGGGAACGCCGCGACTTTGTGGGTTCATTC 1544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGTGGCCATGCGGAGGTACATCGAGAAATCCGGAGGGGAACGCCGCGACTTTGTGGGTTCATTC 840

Qy   1545 CGCCACGGGCACGGATGGCTAATGCGTTGCCTCATGC 1579
          ||||||||||||||||||||||||||||||||||||
Db    841 CGCCACGGGCACGGATGGCTAATGCGTTGCCTCATGC 875
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Search completed: January 15, 2005, 14:58:22
Job time : 1133.56 secs

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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: January 15, 2005, 08:20:57 ; Search time 140 Seconds
                                           (without alignments)
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Title: US-09-965-825-2
Perfect score: 2985
Sequence: 1 MAHSYABQLIDTLEAQGVKR..........GGVGAMIDLIARSNIRNIPTP 579

Scoring table: BLOSUM62
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               Ygapop 10.0 ; Ygapext 0.5
               Fgapop   6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 824507 seqs, 355394441 residues
               Maximum Match 100%
               Listing first 45 summaries

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%

Command line parameters: -DEV=xlh
-MODEL=frame+_p2n.model
-Q=/cgn2.1/USPTO_spool/US09965825/runat_14012005_093021_10313/app_query.fasta_1.775
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-MODB=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09965825 @CGN_1_1_69 @runat_14012005_093021_10313 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -DELEXT=7
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
             1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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             5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1338	1746	4	US-09-543-681A-4139	Sequence 4139, Ap
2	1317.5	1719	4	US-10-096-571-1	Sequence 1, Appli
3	1312.5	1749	4	US-09-489-039A-4884	Sequence 4884, Ap
4	1068.5	1737	4	US-09-252-991A-7335	Sequence 7335, Ap
5	990.5	1448	4	US-10-096-571-8	Sequence 8, Appli
6	948.5	1293	4	US-09-489-039A-4905	Sequence 4905, Ap
7	927	1454	4	US-10-096-571-7	Sequence 7, Appli
c 8	790.5	7900	4	US-08-956-171B-138	Sequence 138, App
9	790.5	7900	4	US-09-781-986A-138	Sequence 138, App
10	749.5	1761	3	US-09-134-001C-1619	Sequence 1619, Ap
11	744.5	2577	4	US-09-252-991A-8458	Sequence 8458, Ap
12	744.5	2754	4	US-09-252-991A-8530	Sequence 8530, Ap

c	13	693	23.2	1113	4	US-09-252-991A-7281	Sequence 7281, Ap
	14	686	23.0	1083	4	US-09-252-991A-7413	Sequence 7413, Ap
	15	643	21.5	1746	4	US-09-107-532A-3181	Sequence 3181, Ap
	16	586.5	21.5	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	17	586.5	19.6	1664976	4	US-09-692-570-1	Sequence 1, Appli
	18	526	17.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	19	521.5	17.5	1701	4	US-09-583-110-1223	Sequence 1223, Ap
	20	521.5	17.5	6211	4	US-08-961-527-8	Sequence 8, Appli
	21	520	17.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	22	516.5	17.3	1947	4	US-09-489-039A-3367	Sequence 3367, Ap
	23	516	17.3	1689	4	US-09-489-039A-840	Sequence 840, App
	24	514	17.2	2111	4	US-10-096-571-11	Sequence 11, Appl
	25	514	17.2	2111	4	US-10-096-571-13	Sequence 13, Appl
	26	514	17.2	2841	2	US-08-452-075-1	Sequence 1, Appli
	27	514	17.2	2841	2	US-09-231-061-1	Sequence 1, Appli
	28	514	17.2	2841	3	US-09-011-762-5	Sequence 5, Appli
c	29	507	17.0	1776	4	US-09-583-110-152	Sequence 152, App
c	30	507	17.0	25002	4	US-08-961-527-48	Sequence 48, Appl
	31	506	17.0	96109	4	US-09-596-002-35	Sequence 35, Appl
	32	493	16.5	2365	1	US-08-363-208-1	Sequence 1, Appli
	33	493	16.5	2365	1	US-09-137-478-1	Sequence 1, Appli
c	34	489	16.4	1710	4	US-09-543-681A-1594	Sequence 1594, Ap
	35	481	16.1	1689	4	US-09-543-681A-199	Sequence 199, App
c	36	466.5	15.6	1755	3	US-09-134-001C-1047	Sequence 1047, Ap
c	37	466.5	15.6	3831	4	US-09-710-279-3959	Sequence 3959, Ap
	38	455	15.2	798	4	US-09-252-991A-7166	Sequence 7166, Ap
	39	449	15.0	1728	1	US-08-403-866-12	Sequence 12, Appl
	40	449	15.0	2231	1	US-08-403-866-14	Sequence 14, Appl
	41	449	15.0	12720	1	US-08-403-866-11	Sequence 11, Appl
	42	448	15.0	1969	1	US-07-737-851-3	Sequence 3, Appli
	43	447.5	15.0	1665	3	US-09-134-001C-1565	Sequence 1565, Ap
	44	447.5	15.0	1665	4	US-09-710-279-1413	Sequence 1413, Ap
	45	447.5	15.0	4093	4	US-09-710-279-3793	Sequence 3793, Ap

ALIGNMENTS

RESULT 1
US-09-543-681A-4139
Sequence 4139, Application US/09543681A

; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4139
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4139

Alignment Scores:
Pred. No.:   4.54e-139
Score: 1338.00
Percent Similarity: 65.55%
Best Local Similarity: 47.80%
Query Match: 44.82%
DB:

Length:	1746	Matches:	272
Conservative:	101	Mismatches:	190
Indels:	6	Gaps:	6

US-09-965-825-2 (1-579) x US-09-543-681A-4139 (1-1746)

Qy   6 AlaGluGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArgIleTyrGlyLeuVal 25
            ||| ::: |||||||| |||:::
Db   40 GCAACCTATATTGCTAAAAGTGCTCAATAATGCAGGTGTGAAACGTATTTGGGGGTGACG 99

Qy   26 GlyAspSerLeuAsnProIleValAspAlaValArgGln---SerAspIleGluTrpVal 44
            ||||||||||||| |||||||| |||:::

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Qy    100 GGCGAATTCAATTGAATGATTAGAGCTTGCCGAAAATGGGTACCCAATTGAATGGAT 159

Qy     45 HisValArgAsnGluValLeuAlaLeuAlaIleAlaPheAlaLeuGluSerLeuIleThrGly  64
          ||||:::|||
Db    160 GGCACACGCCATGAGAAGTCGCGCGCTTTTGCCGCCGAGGCGAGAGCGGCTATCAATGGT 219

Qy     65 GluLeuValAlaCysAlaAlaSerCysGlyTyrProGlyAsnThrHisLeuIleGlnGlyLeu  84
          ||||:||
Db    220 GAATTAGCGCGTTTGTCGCCGGCACCAGGTAACTTACACTTAATTAAAGGACTT 279

Qy     85 TyrAspSerHisArgAsnGlyValAlaLysValLeuAlaLaSerHisHisIleProSerAla 104
          |||:::|
Db    280 TTTGATTGTCATCGTAATCATGGTGTTGCCTGGTTAGCGAGCCATCATATTCCCTCTGCT 339

Qy    105 GlnLeuGlySerThrMetAlaGlyValValSerValValIleProGlyLeuPheGlyTyr 124
          |||||:::||
Db    340 GAAATTGGTAGTACTAATGCTGGTGTTGTCTCAGTAGTTATTCCGGGATTGTTTGGGATAT 399

Qy    125 GlyTyrTyrCysGluMetValAsnGlyValGlyGluGlnGlyArgIleLeuGluHisHisAla 144
          ||::::|
Db    400 CACTATTGTGAATAGTTAGTTCTAAGTCCCGATCAGATCCCACAAAATTCTGAATGTAGT 459

Qy    145 GluAspAlaGlyAlaAspGlyTyrSerAsnSerGlyThrProValVal 164
          ||:||
Db    460 CGCACCCGTCATTTGAAAAGGGCTGTTGCCGTGCCTATTACCCGTGATTAGCGTTA 519

Qy    165 GluAspAlaGlyAlaAspGlyTyrSerAsnSerGlyThrProValVal 184
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Db    520 AAACCCGTCCAGAGAGTGCCCATGAAAAT---TGGTATCCACTACAATCAACCACTGATT 576

Qy    185 PheProAspProThrGlyLeuAlaIleAlaLeuValGlyLleuAlaIleLeuAsnAlaLeuSerVal 204
          ||||::||
Db    577 ATGCCGGAATCGTTTTGAAAATCGAAAAAAACTGTCTGAGCGCACTGAAATAACGCTAAAAATATC 636

Qy    205 ThrLeuPheCysGlyIleAlaGlyValLysAsnAlaArgAlaGlyInValLeuGluAlaGlu 224
          ||||::|
Db    637 ACCTTAATGTGTGGTGCGGTTGTGCTCAAGCACAATGAGTGGTGAAACTAGCACA 696

Qy    225 LysIleLysSerProIleGlyHisAlaLeuGluGlyHisTyrIleGlnHisGlnAsn 244
          |||:::||
Db    697 ACCTTAAAAGCCCCTGTTGTCCACTACGTCGGGAAAGAGTATCTGAGTGGAATAAT 756

Qy    245 ProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyValAlaCysGlyValAlaSerAsn 264
          ::::|
Db    757 CCATGTAGCGTGGGGAATGACGGGCTCTTATCGGTTTTCATCGGGGTTATCACGCAATGAG 816

Qy    265 GluAlaAspLeuLeuIleLeuGlyThrArgAspPheProTyrSerAspPheLeuPro--- 283
          |||
Db    817 AATGCCGTACTTTAGTCGTTGTACTCCGGTACTCCAATTCCCTTATCCGGCTTTCTATCCTCGC 876

Qy    284 LysAspAlaAsnValAlaLaAspIleAsnGlyValAlaHisIleGlyTyrArgArgThrArgVal 303
          ||||::|:||
Db    877 AAAGCTAATATTATTCAAGATATTGACCTTAACGTAGTATTGGCTACATGTCCCATGTG 936

Qy    304 LysTyrTyrProValThrGlyIleGluAlaAsnIleLeuLeuGluValAlaGlu 323
          ||||::
Db    937 GATATGGCTTTGTTGTGGAGATGTCAAAGCAACCCTTAATGCAATTACAACCCGGATTAAAA 996

Qy    324 GluLysThrAspArgSerPheLeuAspArgMetLeuLysLysAlaHisGluArgGlyLeuSer 343
          |||||
Db    997 GAGAAAAAAACAGATACCGCACATCTTGATCGCTGTTAAAA---CATTATGCTAAAGAAGCGC 1053

Qy    344 SerValValGluLeuThrTyrThrHisLysAsnValGluHisValProHisGluTyr 363
          ||||:::||
Db   1054 AAAGATTTAGATGACGATTGGCTCAACCTAGTGACGGTGAGTTG---ATCCACCCTTCAGTAT 1110

Qy    364 ValAlaSerIleLeuAspGluLeuAlaAspLysSerAspAlaValPheThrValAspProThrGly 383
          |||:::|
Db   1111 TTAGCACGTTCGATTTAAGTGAATTAGCCAACGATGGGTATTTTACCTGTTGATCCGATTGGC 1170

Qy    384 MetCysAsnValTrpHisSerAlaArgTyrIleGluGlyAsnProGluGlyThrArgAspPheVal 403
          |||:::|
Db   1171 ACGCCAACAGTTTGGGCAGCACAGTTACGTGAAA---ATGAATGGTAAAACGTCGTTTAATT 1227

Qy    404 GlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleAlaGlnSer 423
          |||:::||
Db   1228 GGTTCATTTAACCATGGTACGATGGCCAATGCATTGCCGCATGCCATTGCTCAAGCA 1287

Qy    424 ValAspArgAsnArgGlnValIleIleAlaMetCysGlyAspGlyGlyLeuGlyMetLeuLeu 443
          ::::|
Db   1288 CTGGACAGAAAACGTCAAGTTGTCATCGCGATGTGCGGTGACGGTGGATTGGGTATGCTGTTG 1347

Qy    444 GlyGluLeuLeuThrValLysLeuHisGlnIleLeuProLeuLysAlaValValPheAsnAsn 463
          ||||:::|
Db   1348 GGTGAATTCATCTCAGTCAAATTGCATCAAATTCTACCGCTGAAAGTGGTGGTGTTTAATAAC 1407

Qy    464 SerSerLeuGlyMetValLysLeuGluIleMetLeuGlyLysValGlyProGluGlyTyrThr 483
          ||||:::|
Db   1408 AGCGTATTAGGTTTTGTGGGCCATGAAATGGTTAGGTAAAGTTGGGCAAGAACTTACCGGTACC 1467

Qy    484 AspHisGluGluLeuValAsnPheAlaGlyIleAlaLaAlaAlaGlyTyrIleLysSerValArg 503
          |||
Db   1468 GATTTCATAATCCTGATTTTGCCCTATTGCCAAATGCGCTGCGCGGCGGGGTATATTAAAAGTGTAGAA 1527

Qy    504 IleThrThrAspProGlyLysLeuAlaGlnIleLeuAlaLeuAlaGlyTyrIleLeuGlyPro 523
          |||
Db   1528 GTTGAGAAAGCGCGAAGATCTTGATGCAAATGGCCTTTGAACAGTAGATGATGGGCCCT 1587

Qy    524 ValLeuIleAspLleValThrAspProAsnAlaLeuSerIleProProThrIleThrTrp 543
          |||:::||
Db   1588 GTTATTGTGGATGGGTTGGTAACCGCAAAACAAGAGCGTTTCCATGCCTCCGGAAATTATTT 1647

Qy    544 GluGlnValMetGlyPheSerLysAlaAlaThrArgValPheGlyValGlyGly 563
          ||||::
Db   1648 GAGCAGGTCCAAAGGTTTTAGCTTGTGATGATTATGATGGCGGATTAATTAAGGGTCGTGTGCGGAT 1707

Qy    564 AlaMetIleAspLeuAlaArgSerAsn 572
          :::||:
Db   1708 GAAATAGTGCAATTAGCCGAAAACCAAC 1734
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RESULT 2
US-10-096-571-1
; Sequence 1, Application US/10096571
; Patent No. 6623944
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 1
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1716)
; OTHER INFORMATION:
US-10-096-571-1

Alignment Scores:

Label	Value	Label	Value
Pred. No.:			
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Percent Similarity:	1317.50	Matches:	266
Percent Identity:	64.81%	Conservative:	106
Best Local Similarity:	46.34%	Mismatches:	195
Query Match:	44.14%	Indels:	7
		Gaps:	6

US-09-965-825-2 (1-579) x US-10-096-571-1 (1-1719)

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Qy   21   IleTyrGlyLeuValGlyAspSerLeuAspAlaVal---ArgGlnSer 39
            ||:||||||::|||||||||| |||| |:: ||| ||
Db   61   ATCTGGGGAGTCACAGGCGACTCTCTTGAACGGTCAGTGTTAATCGCATGGGC 120

Qy   40   AspIleGluTrpValHisValArgAsnGluGluAlaAlaPheAlaLeuAlaGlyGlu 59
            ||| || :::
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Qy   60   SerLeuIleThrGlyGluLeuValAlaCysAlaSerCysGlyProGlyAsnThrHis 79
            :::   ::|:||||||||||||||||||||
Db   181   GCACAACTTAGCGACGGAGAACTGGCCGGGTTCGCGGCCGGGCCCCGGCAACCTGCAC 240

Qy   80   LeuIleGlnGlyTyrAspSerHisAlaArgAsnGlyValCysAlaAlaLeuAlaSer 99
            ||||||||||||||||||||||:::
Db   241   TTAATCAACGGCCTGTTCCATCGGCGACTCACGTTGCCACGGCGACTTCCGGCT 300

Qy   100   HisIleProSerArgAlaGlnIleIleGlySerThrHisProGluIleLeu 119
            ::||: ||| || || |: ::
Db   301   CATATTCCCCAGCGAAATTGGCAGCTATTTCCAGGAAACCCACCCAGAGCTA 360

Qy   120   PheLysGluCysSerGlyTyrTyrCysGluMetValAsnGlyGlnGluArgIle 139
            |||::   ::| ||| :::
Db   361   TTCCCCGAATGAGTAGCTCACTATTCCAGCCCGGAGCAGATCCCACAAGTA 420

Qy   140   LeuHisHisAlaIleGlnSerThrMetAlaGlyTyrGlyValSerValValIlePro 159
            |||||||||||:||||||||||||||||
Db   421   CTGGCGCGGATTCCCATCGCAAAGCGGTGCTTTAACCCTGGCCGTTTCGTGTTACCA 480

Qy   160   GlyAspIleAlaLysGlyAspAlaGlyAlaGlyThrTyrSerAsnSerThrIleSerSer 179
            ||| || ||
Db   481   GGCGACGTGCGCGTTAAAACCTGCGCCGCAGAAGGGGCA---ACCATGCAC 537

Qy   180   GlyThrProValValPheGluProAspThrGluAlaAlaAlaLeuValGluAlaIleAsn 199
            |||| ||| || :: :::
Db   538   CCACAACCAGTCGTCGACGCCCGAAGAGAAGAGTTACGCAAACTGGCCGCCAACTGCTGCGT 597

Qy   200   AsnAlaLysSerValThrLeuPheCysGlyAlaGlyValLysAsnAlaArgAlaGlnVal 219
            :::   :::   ::: |||
Db   598   TATTCCAGCAATATCGCCCTGATGTGTGGCAGCGGCGCTGCCGCGGGCCGCATAAAGAGTTA 657

Qy   220   LeuGluLeuAlaGluLysIleLysSerProIleGlyHisAlaLeuGlyValGlyGlnThrTyr 239
            :::||::||||||||||||||||||||||||||:::
Db   658   GTTGAGTTGGCCGGGAAAATTAAAGCCCCTATTGTTCATGCCCTTGGCGTGGGTTAAAGAACAT 717

Qy   240   IleGluHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyValAlaCys 259
            ||| :::|| ::|||||||||||| ||||| ||||||
Db   718   GTCGGAATACGATAATCCGTATGAGTGTGGAATGACCGGGTTAATCGGGTTCTGGTGTCAGGT 777

Qy   260   ValAspAlaSerAsnGluValAlaAspLeuLeuIleLeuLeuGlyThrArgAspPhaProTyrSer 279
            || ||||:||||||| || |||
Db   778   TTCCATACCATGATGAACGCCGACACGTTAGTCGCTACTCGGCACGCCGCAAATTCCCATACCG 837

Qy   280   AspPheLeuProLysAsp---AsnValAlaGlnIleAsnGlyAlaHisIleGly 298
            |||||||||||::: ||||:::|||||||||||
Db   838   GCCGCCTTCACCCGACCGCCGCAAAATCATTCAGATGAATATCAACCAGCCATCGGC 897

Qy   299   ArgArgThrHisThrValLysTyrProValThrGlyAspValAlaLeuThrIleGluAsnIle 318
            |||||||:::
Db   898   GCTCACGCACCAAAGGTGGATATGGCACTGGTCGGCGATATCAAGTTCGACTCTTGCGTGCATTG 957

Qy   319   LeuProHisAlaValLysGlyGluLysTyrThrAspArgMetLeuLysAlaHis 338
            :::|||||||||||:|||||:::||||||||||||||||:::
Db   958   CTTCCATTGGTGGAGAAAAAGCCCATCGCAAGTTCTCGGATAAAGCGGCTGGAAGATTAC 1017

Qy   339   GluArgLysLeuSerSerValValGluThrTyrThrHisAsnValGluValHisValPro 358
            :::::||||||||||||||||||||||
Db   1018   ---CCGGACGCCCCGCCAAAGGGCCTTGGACGATTAGCTAAACCGAGCCGAGAA------GCC 1068

Qy   359   IleHisProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPhe 378
            ||| ::: |||||| ||| |||
Db   1069   ATTCACCCGCAAATATCTGGGCCCAGCAAAATTAGTCATTTTGCCGCGATGAGGCTATTTC 1128

Qy   379   ThrValAlaAspThrGlyMetCysAsnValTrpHisSerAlaAlaArgTyrIleGluAsnProGluGly 398
            ||| |||||| |||
Db   1129   ACCTGTGAGACGTTTGGCCCAACGTGTGGGCCCGCAGCGTTATCTAAAA---ATGAAACGGC 1185

Qy   399   ThrArgAspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAla 418
            :::||||||||||
Db   1186   AAGCGTCGCCGCCTTGGTGTTAGGTGGCGTTCGATTTAACCACGGTTCGAATAGCGCCGCAGGCG 1245

Qy   419   IleGlyValAlaGlnSerValAspArgAsnArgGlnValIleGlnAlaAlaLeuAlaGly 438
            |||:::   :::   ::: |||
Db   1246   CTGGGTCGCGACGAGCTGGACGAACGTCAGGTGGTGCCGGCCGGCCTGGTCGCGGGTGGGT 1305

Qy   439   LeuGlyMetLeuLeuGlyIleLeuGluThrValLysLeuGluHisGlnLeuProLeuGluAla 458
            |||||| |||::
Db   1306   TTTAGCATGTTGCAGGGCGACGAGGTCGCAGGTTCGCCGCTGGCGGCGGCGCTGGTG 1365

Qy   459   ValValPheAsnAsnSerSerLeuGlyMetValLysGluLeuGluVaValGlyGln 478
            ||||| :::|||||||||||
Db   1366   GTCGTCTTTAACAACAGCGTCGTGGGCATGGTGAAACTGCCGCGAGTGATGGTG 1425

Qy   479   ProGluPheGlyThrArgAspHisGlyValAsnPheAlaGlyIleIleLeuAlaAlaGly 498
            ||| |||:::   ::|||
Db   1426   TTGACTCGACGGCACACGGAACTACACGACAAACTTTGCCCCATTGCCGAAGCGTGCGGC 1485

Qy   499   IleLysSerValArgIleThrAspProLysGlyValArgGluValGlnLeuAlaLeu 518
            ||| :::   :::||| ||||||
Db   1486   ATTACGGGTATCCGTGTGAGAAAAAGCCTCTGAAGTGATGAGCCCGCCTTC 1545

Qy   519   AlaThrTyrProGlyProValLeuIleValIleThrArgAspProAsnAlaLeuSerIlePro 538
            ||| ::: ||||||
Db   1546   TCCATCGACGGTCCGGTTGTGGTGGAGATGAGAGAGTTAGCCGCCATTCCA 1605

Qy   539   ProThrIleThrTrpLysGlnValMetGlyPheSerLysAlaAlaThrArgProValPhe 558
            ||| ::||| ||| ::: |||
Db   1606   CCGGCAGATCAAAACTCGAACAGCCCAAAGGTTTCAGCCTGTTATAATGCTCGCCAATCATC 1665

Qy   559   GlyGlyGlyValGlyAlaMetIleAspProLeuAlaArgSerAsn 572
            :::||||||||| :::|||||||||||
Db   1666   AGCGGACGGCGGTGATGAAGTGATCGAACTGGGCGAAACAAAC 1707

Alignment Scores:
Pred. No.:
Score: 3.19e-136
Score: 1312.50   Length: 1749
Percent Similarity: 64.63%   Matches: 266
Percent Identity: 46.34%   Conservative: 105
Best Local Similarity: 43.97%   Mismatches: 196
Query Match: 4   Indels: 7
DB: Gaps: 6
US-09-965-825-2 (1-579) x US-09-489-039A-4884 (1-1749)

```
Qy    1 MetAlaHisSerTyrValAlaGlyGlnLeuIleAspThrLeuGluIleAspGlnGlyValLysArg 20
        |||                                                            ::: ||
Db 1099 ATTCACCCGCCAATATCTCGGCCGCAGGCAGCAGATCAGTCAGTTTGCCGATGAAGATGCCATTTTC 1158

Qy   21 IleGlyLeuValGlyAspSerLeuAsnProIleValAspAlaVal---ArgGlnSer 39
        ||                                      :::                 :::
Db 1159 ATTCTGGGGGCGGTCACCCGAGAATCCCTCAATGGATTGAGGATAGCCTTAACCGCATGGC 1215

Qy   40 AspIleGluTrpValHisValArgAsnGlyLeuValAlaLeuAlaPheAlaLeuGlyAlaGlu 59
        ||                                                           |||
Db 1216 AAAACGCCCCTTCGGTCTGGGCTCGTTCAACCACGGCTCAATGCCGACACGCCCCAGGCC 1275

Qy   60 SerLeuIleThrGlyGluLeuAlaLysAlaSerCysGlyProGlyLysAsnThrHis 79
        ::::                                                    :::
Db 1276 ATCGGCGCCAAGGCCACTGCGCGCCGAGCGCGGCTAGTAGCCCATCTGCGCGGCGGGG 1335

Qy   80 LeuIleGlyLeuTyrAspSerHisArgAsnGlyAlaLysValLeuAlaIleAlaSer 99
        :::                                                     :::
Db 1336 TTCAGGATGCTGGATGCGCAGTCGGGATTTCTGTCGCCCGGCGGGCAGGAGATT 1395

Qy  100 HisIleProSerAlaGlnIleIleGlySerThrArgHisHisProGluIleLeu 119
        |||                                                 :::
Db 1396 CACATCCCATCCCAGGAAAATCGGCTACCTCATTCCGCCGGTGCGCGGCAGA 1455

Qy  120 PheLysGlyCysSerGlyTyrCysGlyIleGlnGlyGluGlyIle 139
        :::                                       :::
Db 1456 CTCACGACCGTACCGAGCTCCACGATACCAACCTTCGCCGCGA 1515

Qy  140 LeuHisHisAlaIleGlnSerThrMetAlaGlyValSerValValValIlePro 159
        |||                                                 :::
Db 1516 ATCAAAGGGTTAACGAACAGCGTTCGTCGGACGTGGATGAAGCGGTTCCAGA 1575

Qy  160 GlyAspIleAlaLysGlyAspAlaGlyAlaGlyTyrTyrSerAsnSerThrIleSerSer 179
        |||                                                      :::
Db 1576 CGCACCGACGGTTCCGGTGCGGTCGACGTCGTCGTGGGCCAAAGAGAACTG 1635

Qy  180 GlyThrProValPheProAspProThrGlnAlaAlaAlaLeuValGluValIleAsn 199
        |||                                                    :::
Db 1636 CCGCAGGATCAAGTCGAGCGGCCAAAGGCTTTAGCCTGTATATGTCGCGGCGGCGATC 1695

Qy  200 AsnAlaLysSerValThrLeuPheCysGlyAlaGlyValAspAsnAlaArgAlaGlnIleVal 219
        :::                                                          :::
Db 1696 AGCCGGCGGCGGCCGATGAGGTCATCGACGGCCAAAACCAAC 1737

Qy  220 LeuGlyLeuAlaGlyLysSerProIleGlyTyrHisAlaLeuGlyLysGlnTyr 239
        :::                                                :::
Db  688 GTGGAGTTCGGCAGCCAAAAATTAAAGCCCCACCGCTGGGATTGGG 747

Qy  240 IleGlnHisGluAsnProPheGlyValGlyMetSerGlyLeuGlyTyrGlyValAlaCys 259
        |||                                                     :::
Db  748 GTGGGAGTACGGACAACCCGTACGATGTGGGCATGAGCGGGCTCGTTCTCTCTGGC 807

Qy  260 ValAspAlaSerArgGluAlaLeuAspLeuLeuLeuGlyLeuThrAspPheProTyrSer 279
        |||                                                      :::
Db  808 TTCCACACCATGATGAACGCGATACCCGATCCCAGTTCCCCTATCGC 867

Qy  280 AspPheLeuProLysAsp--AsnValAlaAspIleAsnGlyAlaHisIleGly 298
        |||                                               :::
Db  868 GCCTTCTTACCACCGACCGAAAATTATTCCAGATGCAGCATCAACCCCGAGCATCGC 927

Qy  299 ArgArgThrArgValLysTyrProValThrGlyAspValAspThrLysGluAsnIle 318
        |||                                                    :::
Db  928 GCACACAGTAAGGTCGACATGGCCCTGGTGTGGGGCGTAATAAATCGACCTGAAAGGCCTG 987

Qy  319 LeuProHisGluValLysGlyGluThrAspArgMetLeuLysValAlaHis 338
        |||                                             :::
Db  988 CTGCGCGCTGCTGGAGGAAGAGAGAAAAACCGATACCCACACTTCCTGCGA 1044

Qy  339 GluArgLysLeuLysSerSerValValGluThrTyrThrHisAsnValGluLysValPro 358
        |||                                                     :::
Db 1045 TATCGACGACGGCGGGAAAAGGGCTCGACGATCTCGGCTAAAACCAGACGGATAAA 1098

Qy  359 IleHisProGluGlyTyrValAlaSerIleLeuAsnGluLeuAlaAspLysAspAlaValPhe 378
        |||                                                        :::
Db 1045 ...
```

Alignment Scores:
Pred. No.:
Score: 5.37e-109
Percent Similarity: 1068.50
Best Local Similarity: 61.15%
Query Match: 40.47%
                            35.80%

Length:	1737	
Matches:	225	
Conservative:	115	
Mismatches:	207	
Indels:	10	
Gaps:	5	

US-09-965-825-2 (1-579) x US-09-252-991A-7335 (1-1737)

```
Qy      6 AlaGluGlnLeuIleAspThrLeuGluGlnGlyValLysArgIleTyrGlyLeuVal 25
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     47 GCCGGAGATCCGTTGGAAACCCTGGAAGCCCGGGTTCCGCATTGCTARGGCATCGTC 106

Qy     26 GlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAspIleGluTrpValHis 45
            |||||||||            |||||||||||||   :::     ||||||
Db    107 GGCGGACACCCTCAACCATGTCACCGACGGATCCATCGAGATCCAGTGGGTCCAC 166

Qy     46 ValArgAsnGluGlyLeuAlaAlaAlaAlaPheAlaAlaGlyTyrAlaArgGlyGlyGlu 65
            |||:::||||||||||||||||||||||||||||||||:::||||||||||
Db    167 GTGCGCGCCAACGAAGGGCCCTTCGCCGCCGCGGGAGTCCTACATCAGCGC 226

Qy     66 LeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeuIleGlnGlyLeuTyr 85
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    227 CTGACCGCTGCGCCTCCTGCGGACGCTTCATCAACGGGCTTAC 286
```

(... alignment continues ...)

```
Qy    345 ValValGluthrTyrThrHisAsnValProIleHisProGluTyrVal 364
            :::   ::: ||||||||||||||||||||||||||:::::::::
Db   1051 CTGGAAAA-------GAGGAGCAAGCCGGAGCCGGAGTCGATCCATCCGCAGCACCTG 1104
```

RESULT 5
US-10-096-571-8
Sequence 8, Application US/10096571
Patent No. 6623944
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DE 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 1448
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Start codon of the delta poxB allele
; NAME/KEY: misc feature
; LOCATION: (1)..(605)
; OTHER INFORMATION: 5' region of the delta poxB allele
; NAME/KEY: misc feature
; LOCATION: (606)..(674)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc feature
; LOCATION: (675)..(1445)

```
;  OTHER INFORMATION: 3' region of the delta poxB allele
;  NAME/KEY: misc_feature
;  LOCATION: (1446)..(1448)
;  OTHER INFORMATION: Stop codon of the delta poxB allele
US-10-096-571-8

Alignment Scores:
Pred. No.:

Score:                990.50          Length:           1448
Percent Similarity:   54.45%          Matches:           228
Best Local Similarity: 39.79%         Conservative:       84
Query Match:          33.18%          Mismatches:        166
DB:                   4               Indels:             96
                                      Gaps:               10

US-09-965-825-2 (1-579) x US-10-096-571-8 (1-1448)

Qy      1 MetAlaHisSerTyrAlaGlnGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArg 20
            ||||||||||||||||||||||||  :::
Db      1 ATGAAAACAACCGGTTGCAGCTTATATCGCCGAATCGGGAGGGGTGAAACGC 60

Qy     21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaVal---ArgGlnSer 39
            |||:|||:|||  ||:                                :::
Db     61 ATCTGGGGAGTCAACAGGCCACTCTCTGAACGGGTCTTAGTGACAGTTCTTAATCGCATGGAC 120

Qy     40 AspIleGluTrpValHisValArgAsnGluGlnValAlaAlaAlaPheAlaAlaAlaGlyAlaGlu 59
            :::      ||||:||||||||||||:::
Db    121 ACCATGGAGTGGATGCCACCCCACGAAGAAGTGGCGGGCCTTTGCGGGCCTGGAA 180

Qy     60 SerLeuIleThrGlyLeuGluAlaValCysAlaAlaSerCysGlyProGlyAsnThrHis 79
            |||:|||:|||  ||:
Db    181 GCACAACTTAGCGAGAACTGGCGGCTCGGCCCCGGGGTTCCCCCGGGCCCCAACTGCAC 240

Qy     80 LeuIleGlnGlyLeuTyrAspSerHisLeuArgAsnGlyLeuLysValLeuAlaIleAlaSer 99
            ||||:||||  ::
Db    241 TTAATCAACGGCCTGTTCGATAGTCACCTGCGTAACGGTCTGAAAGTTCTGGCGATTGCCTCT 300

Qy    100 HisIleLeuProSerArgAlaGlnIleLeuGlySerThrPhePheGlnLeuThrThrHisProGluIleLeu 119
            ||||||||||||||||||||  ::
Db    301 CATATTCCCTCCCAGGCGAAATTGCAGGGCTCTACTTTCCAGCAAACCACCACACAGAGCTA 360

Qy    120 PheLysGluCysSerGlyTyrCysGluMetValAsnGlyValGluGlyArgIle 139
            ||||||||||||
Db    361 TTCCGCGAAATGTAGTCACTATTGCGACCTGGTTTCCAGCCCGGAGCAGTA 420

Qy    140 LeuHisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValValValIlePro 159
            |||||||||||||||||:||  ::
Db    421 CTGGCCGATTGCCATGCCAAAGCGGTGCTTAACCGTGGCGTTTCGGTTGTGTGTTACCA 480

Qy    160 GlyAspIleAlaLysGluAlaProAlaGlyLysTyrTyrSerAsnSerThrIleSerSer 179
            ||||||||:|||:||||||  :::
Db    481 GGCGACGTGGCGGTTAAAACCTGGCGCCAGAGGGGCA---ACCATGCACTGGTATCATGCG 537

Qy    180 GlyThrThrProValValPheProAspProThrGlnAlaAlaIleAlaLeuValGluAlaAsn 199
            ||||  ::
Db    538 CCACACACCAGTCGTGCACCCGGAACGAGAGGAGTTACGCAAACTG 582

Qy    200 AsnAlaLysSerValThrLeuPheCysGlyValGlyAlaGlnVal 219
            ----GCGCCAACTG
Db    583 ----

Qy    220 LeuGluLeuAlaGluLysSerProIleGluGlyHisAlaLeuGluGlyGlyLysGlnTyr 239
            ||||  :::||||||
Db    592 CTG------CGTTAT

Qy    240 IleGlnHisGluAsnProGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCys 259
            :::  :::
Db    601 TCCAGGCCTAAGGCGCGAATTCCAG------

Qy    260 ValAspAlaSerAsnGluValAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyrSer 279
            ------

Db    624 ------
Qy    280 AspPheLeuProLysAspAsnValAlaGlnValAlaAspIleAsnGlyAlaHisIleGlyArg 299
```

(right column)

```
Db    625 ------
Qy    300 ArgThrThrValLysTyrProValThrGlyAspValAlaLeuAlaThrIleGluAsnIleLeu 319
            |||                                               |||    |||
Db    637 CGTTA-CTAGTCGGAT---CCGGATCTGCAGAATTC---GCCCTTCTGCCTGCATTGCTT 636

Qy    320 ProHisValLysGlyLysThrAspArgSerPheLeuAspArgMetLeuValAlaHisGlu 339
            |||  ::||||||||||||:||
Db    690 CCATTGGTGGAGAAAAGCCCGATCCGCAAGTTTCTCGGATAAAGCCGCTGGAAGATTAC--- 746

Qy    340 ArgLysLeuSerSerValValGlyLysValGluThrTyrThrHisAsnValGlyHisLysValProIle 359
            :::::
Db    747 CGCGAGCGCCCGCAAGGCGTCGGACGATTTAGCTAAAACCGAGCGAGAAA------ 800

Qy    360 HisProGluThrTyrAlaValAlaSerIleIleLeuAsnGluLeuAlaAspLysAspLysPheThr 379
            |||||||||||||||  :::
Db    801 CACCCGCAATATCCTGCGCGACCAGCAAATTAGTCATTTTGCCGATAACGGCTATTTCACC 860

Qy    380 ValAspThrArgGlyMetCysAsnValAlaTrpHisAlaArgTyrIleLeuGluAsnProGluGlyThr 399
            |||||||:||||||||||:|||
Db    861 TGTGACGTTGGTGGTACGCCAACCGGTGTGGGCGGGCCACGTTTACTGCTGGAAAATCCGGAAGGTACG 399

Qy    400 ArgAspPheValGlySerPheAlaArgHisSerGlyThrMetAlaLeuAsnAlaLeuProHisAlaIle 419
            ||||:||||||||||||:||
Db    918 CGTGCGCCTTGGTTAGGTTCGTTTACCAGCCGCCCGTTCCACGCGCTGGCCATGCGCATTATCCAGTGG 419

Qy    420 GlyAlaGlnSerValAspArgAsnArgGlnIleValIleAlaMetCysGlyAspGlyGlyLeu 439
            |||||||||||  :::
Db    978 GGTGCGCAGGCGGACAGACGTGCCGGACCGTTCAGGTGGTCGCGGCGGGCGTTT 1037

Qy    440 GlyMetLeuLeuGlyGluLeuLeuThrValArgLysLeuGlyIleLeuProLeuLysIleAlaVal 459
            ||||:::|||||||||  ::
Db    1038 AGCAGTTGATGGGCGAATTCCTCAGTGAGTGCGAGAGAAACTGCCAGTGAAAAATTGTC 1097

Qy    460 ValPheAsnAspAsnSerSerLeuGlyLeuGlyMetLysLeuValGlnGlyLeuPheLysPro 479
            |||  :::||||||
Db    1098 GTCTTTAACGACACGCGTGCTTGGGCTTGGTTATGAAGCTGGTGGTCGGCAATTG 479

Qy    480 GluPheGlyValThrAspHisGlnValAsnPheAlaGlnLeuIleAlaAlaLeuAlaAla 499
            ||||||||||||||  :::
Db    1158 ACTGACGGCGACCGAACTACACGACACAAAACTTTGCCGCCAATGCCGAAGCTGGCG 1217

Qy    500 LysSerValArgIleThrAspProLysGlyLysLeuValAlaAspGlnGlnAlaAlaAlaAla 519
            :::  :::
Db    1218 ACGGGTATCCGTGCTGATGAAAAACGTTCGAAGTTGATGAAGCCCGCGCCTTCTCC 1277

Qy    520 TyrProGlyProValLeuLeuAspIleValThrAspProAsnAlaLeuSerIleProPro 539
            |||  :::
Db    1278 ATGGACGGTCCGGTGTTGGTGGATATTGTGGTCGGCAAGAGAGGTTAGCCATTCCACCG 1337

Qy    540 ThrIleThrTrpProGlnValMetGlyPheSerLysAlaAlaAlaThrArgThrValPheGly 559
            |||  :::
Db    1338 CAGATCAAAACTCGAACAGGCCAAAGGTTTCAGCCTGTATAATGCTGGGCGCAATCATCAGC 1397

Qy    560 GlyGlyValGlyAlaMetIleAspGlnLeuLeuAlaAlaArgSerAsn 572
            :::||||  ::||:||||||||  :::||
Db    1398 GGACGCGGCTGATGAACTGGCCGAAAACAAAC 1436
```

(lower right)

```
RESULT 6
US-09-489-039A-4905/c
; Sequence 4905, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
```

; SEQ ID NO 4905
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4905

Alignment Scores:
Pred. No.:
Score: 8.13e-96
Percent Similarity: 65.69%
Best Local Similarity: 46.47%
Query Match: 31.78%
DB:

```
                                              Length:          1293
                                              Matches:          191
                                              Conservative:      79
                                              Mismatches:       134
                                              Indels:             7
                                              Gaps:               6
```

US-09-965-825-2 (1-579) x US-09-489-039A-4905 (1-1293)

```
Qy    1  MetAlaHisSerThrArgLeuGlyGluGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArg  20
            |||||||              ::: :|||  ||    |||||  :|::
Db 1218  ATGAAAACAGCCGTGCGGCATAACATTGCCAAAACGGTTGGACAGGCGGGTGAAACGT  1159

Qy   21  IleTyrGlyLeuValGlyAspSerHisLeuAsnProIleValAspAlaVal---ArgGlnSer  39
            ||| :|||:||||||:::||||:::|||  | ||        |||  :::        |||
Db 1158  ATCTGGGCCGGTCACCGGAGATTCCCTCAATGGATAGCCTTAACCGACATGGGC  1099

Qy   40  AspIleGluTrpValHisValArgAsnGlyValAlaAlaAlaPheAlaAlaAlaGlyAlaGlu  59
            |||||  :::|||:||:|:|  ||||||||||::::|||||||||||||:||
Db 1098  ACCATCGACTGGATGCCACCCGGACGAAGAGGTCGCCGGCTTTCGGCGCCGGAA  1039

Qy   60  SerLeuIleThrGlyLeuLeuValAlaValCysBAlaAlaSerCysBGlyProGlyAsnThrHis  79
            :::        |||||||||||||||   ::: ||||||||||||      |||
Db 1038  GGCGACGTTGACCGGAGCTGGCGGTCTGCGCCCCGGCGTTCCTCCGGACGGGGCAAACCTGCAC  979

Qy   80  LeuIleGlnGlyLeuTyrAspSerHisHisArgAsnGlyAlaLysValLeuAlaIleAlaSer  99
            |||||| |||||||     ||||||  || |||  ||||  |||||||||||||||
Db  978  CTGATTAAACGGTTGTTTGTTGACTGTCACCACCATGTCCCGGTTGGTGTGGGTTGTTGCCC  919

Qy  100  HisIleProSerAlaGlnIleIleGlyHisGluThrHisProGluLeuLeu  119
            |||||||||||||||    ||||| |||  ::: |||   |||||
Db  918  CACATCCCATCCAGCCAGATCGGACGGGGCTATTTTCAGGAAACCCATCCTCAGGAGCTG  859

Qy  120  PheLysGluCysBSerGlyTyrCysBGluMetValAlaAsnGlyValGlyValGlnGlyGluArgIle  139
            ||| :::|||||||   |||   ||||||:||||  ||| |||||||:::
Db  858  TTCCCGGAGTGCAGCCATTACTGCGAACTGGTTGCTCACGCGCCGGAGCAGGATCCCGGAGGTG  799

Qy  140  LeuHisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValValAlaValIleProPro  159
            |||||||||                :::       |||::|||||||||||||||||||
Db  798  CTGGCAGTGGGGCGGATGCCTAAGGCAGTTAACCGCGTGGTTGGTGGTGTTGGTTGCCC  739

Qy  160  GlyAspIleAlaLysGlyValAspAlaAlaGlyAlaGlyTyrSerAsnAlaArgAlaGlnValVal  179
            :::        ||| |||||||       ||| ||||||||||  |||||||||||
Db  738  GGGCGATGTGGGCGCTGAAGGGCCCCCCCGGAAAGCGCC---AGCAGCCACTGGTATCATGCG  682

Qy  180  GlyThrProValAlaPheProAspProThrGluAlaAlaAlaLeuAlaLeuValGlnAlaIleAsn  199
            :::        |||||||::|||||||||||||||||||   ::: ||||
Db  681  CCGCTGCCGACGGGTCACCCCGGCGAAGAGAGCTGCGCGAAGCTGCGCAGCTATTCGC  622

Qy  200  AsnAlaLysSerValThrLeuPheCysBGlyAlaGlyValLysGlyAlaGlnGlnVal  219
            ::: :::        |||||||  |||||| ||||||||||||:::|||
Db  621  TACTCCAGCAATATCGCGTCCCGCCATGTCGGCGGTTGGCGCCCCACCAGGAACTG  562

Qy  220  LeuGluLeuAlaGluGlyLysGluLeuSerProIleGlyHisGlyHisGlnGlnTyr  239
            |||||||||||||||||   :|||||||||||||||||||||||:::
Db  561  GTGGAGTTCGCAGCCAAAATTAAAGCCCCATCGTCCACGGCCCTGCGCGGCAAAGACAC  502

Qy  240  IleGluHisGluAsnProHisGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysB  259
            ::||:|:|||||||||||||||||   |||:::||||||||||||||||
Db  501  ATCGAGCATGAAAACCCTCACGAAGTGGGCATGTCGGGCCTGCTTGGCTATGGCGCTTGC  442

Qy  260  ValAspAlaSerAsnGluLeuLeuLeuLeuGlyThrArgPheProTyrSer  279
            ||||||||||  |||||||||||  |||||:||||||||||
Db  441  TTCCACACCATGAAGATGAACGCCGATACCCTGCTGGGGCCACCCAGTTCCCCTATCGC  382

Qy  280  AspPheLeuProLysAspGlu---AsnValAlaGlnValAlaAspIleAsnGlyAlaHisIleGly  298
            |||||||||||||||   ||||||   :::||||||||||||||||:::
Db  381  GCCTTCTACCGACCGCCGGCGAAAATTATCCAGATCGACATCAACCCCGGCGCAGCCATCGGC  322
```

RESULT 7
US-10-096-571-7
; Sequence 7, Application US/10096571
; Patent No. 6623944

; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: Process for the preparation of D-pantothenic acid and/or salts the
; FILE REFERENCE: 211499
; CURRENT APPLICATION NUMBER: US/10/096,571
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: DB 10112102.4
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/304,776
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1

; SEQ ID NO 7
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1454)
; OTHER INFORMATION: Mutagene DNA
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (57)..(577)
; OTHER INFORMATION: Part of the 5' region (poxB1) of the poxB gene
; NAME/KEY: misc_feature
; LOCATION: (578)..(646)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
; NAME/KEY: misc_feature
; LOCATION: (647)..(1398)
; OTHER INFORMATION: Part of the 3' region (poxB2) of the poxB gene
; NAME/KEY: misc_feature
; LOCATION: (1399)..(1454)
; OTHER INFORMATION: Technical-grade DNA/Residues of polylinker sequence
US-10-096-571-7

Alignment Scores:
Pred. No.:
Score: 2.48e-93
Percent Similarity: 53.28%
Best Local Similarity: 39.42%

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                                              Length:          1454
                                              Matches:          216
                                              Conservative:      76
                                              Mismatches:       156
```

```
Db  204  TATCGCGACGGCGGAAAAGGCTTCGACGATCGTGGCGTAAACCCAGCCATGATAAA--  151

Qy   33  AAACGCCGCCTGCGTGGGTGCTTCGTTCAACCACGGC   1
            :::|  ||||||||   |||||||| |||  |||||||
Db   33                                           1

Qy  399  ThrArgAspPheValGlySerPheArgHisGly  409
            ::: |||  ||||||  ||||||| |||
Db   90  ACCTGTGATGTCGGCCACCCCGACCGTCTGGGCGGGGCACCGCTACTCAAA---ATGAAATGGT  34

Qy  379  ThrValAspThrGlyMetCysBAsnValTrpHisAlaArgTyrIleGluGluAsnProEluGly  398
            ::: |||||||||| |||||||||||  |||||||||||||||||:::
Db  150  ATTCACCCGCAATATCTGGCACGCCAGACGGATCAGTCATTTTGCCGATGAAGAGATGGCCATTTTC  91

Qy  359  IleHisProGluTyrValAlaSerIleLeuGluAsnGlyLeuValAlaAspGlyLysAspAlaValPhe  378
            ::|||||||  ::::||||||||||:::|||  |||||||||||||||:|:|
Db  261  CTGCCGCTGCTGAAGAGAAAACCGATCGCCAGCGATCAGTCAGTCAAGTCATTTTGCCGAT  205

Qy  319  LeuProHisValLysGlyLysGlyThrArgAspArgSerPheLeuLeuAspValAspArgMetLeuLeuLysAlaGlyAlaHis  338
            ||||||||||||  |||||||:::     ||||||   |||||||||:::
Db  321  GCACACAGTCAGGTCGACATGGGCCGCTGGTCGGGCCGGGTTGGGCCGATAATGAAATCGGACGCCTG  262

Qy  299  ArgAlaArgThrThrValLysTyrProValThrGlyAspAlaValAlaAlaIleAlaThrArgIleGluGluAsnIle  318
            ::: |||||||||| ::: |||||||||||:::        |||||||||||||||:::
Db  381  GCCTTCTACCGACCGCCGGCGAAAATTATCCAGATCGACATCAACCCCGGCGCAGCCATCGGC  322
```

```
Query Match:          31.06%      Indels:    101
DB:                      4        Gaps:       10

US-09-965-825-2 (1-579) x US-10-096-571-7 (1-1454)

Qy    25  ValGlyAspSerLeuAsnProIleValAspAlaValAlaGlnSerAspGluTrpVal   44
          |||      |  ||      ||          ||| || |||
Db    66  CTTAGTGACAGTCTTAAT---------------------CGCATGGGACCATCGAGTGGATG  107

Qy    45  HisValArgAsnGlyGluAlaAlaAlaPheAlaAlaGlyAlaGluSerLeuIleThrGly   64
          ||      ::|||         |||   | |||||       |||   ||||||     :::
Db   108  TCCACCCGCCACGAAAGAAGTGGCGGCGGCCTTTGCCGCGGGTGCAGAACTTATAACCGGA  167

Qy    65  GluLeuAlaValCysAlaAlaSerCysGlyPheGlyLeuGlyLeu   84
          ||||              |||    ||||           |||
Db   168  GAACTGGCGGTTCTGCCGCCCCGGACCGCAACCTGCACTATCAACCGCTG  227

Qy    85  TyrAspSerHisArgAsnGlyTyrAlaLysValLeuAlaIleAlaSerHisIleProSerAla  104
          :::          ||   |||    ||||||      |||        |||
Db   228  TTCGATTGCCACCGCAATCACGTTCCGGTACTGGCGATTGCCTCAATATTCCCTCCAGC  287

Qy   105  GlnIleGlySerThrPhePheGlnGluThrHisProGluIleLeuPheLysGluCysSer  124
          |||||  :::          ||||         |||     |||   ::|||
Db   288  GAAATTGGCACGCGGTTACTTCAGGAAACCCACCCGGAAATTCTGTTT  347

Qy   125  GlyTyrTyrCysGluMetValAsnGlyGlyGlnGlyUGlyValGlyIleLeuHisIleAlaIle  144
          ||||||||    |||      |||      |||     :::  |||
Db   348  CACTATTGCGAGTGGTTTCCAGCCCGGAGCAGAATCCCAACTACTGGCCGATTGCCATG  407

Qy   145  GlnSerThrMetAlaGlyValSerValValIleProGlyAspIleAlaLys   164
                ||  :::          ||||||     :::      |||
Db   408  CGCAAAGCGGTGCTTAACCGTGCGTTTCGGTTGTCCGTTACCAGGCGACGGGGGTTA  467

Qy   165  GluAspAlaLeuValAspGlyThrTyrSerAsnSerThrIleSerGlyGlyThrProValVal  184
          :::          ||||    ::    ||           |||
Db   468  AAACCTGGGCACCGGAGAAGGGCA---ACCATGCACTGTGATCATGCGGCCACAACCAGTCGTG  524

Qy   185  PheProAspProThrGluValLeuAlaLeuAlaLeuIleLeuAsnAsnAlaLysSerVal  204
          ||| |||       |||                :::              |||
Db   525  ACGCCGGATGAAGAAGAGTTACGCAAACTG----------------------  554

Qy   205  ThrLeuPheCysGlyValAlaGlyValLysAsnAlaArgGlnValLeuGluLeuAlaGlu  224
          |||||||                ||||||   :::::  |||
Db   555  ---------------------GCGCAACTGCTG------------  566

Qy   225  LysIleLysSerProIleGlyLysGlyThrTyrIleGlyHisGlnAsn  244
          :::||:||                ||||
Db   567  ---------------------CGTTATTCCAGGCCTAAGGGC  587

Qy   245  ProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValAlaSerAsn  264
          |||                ::            |||
Db   588  GAATTCCAG------------------------  596

Qy   265  GluAlaAspLeuLeuLeuLeuGluGlyThrAspPhePheProTyrSerAspPheLeuProLys  284
          |||                |||
Db   623  ---CCGAGATCTGCAGAATTC---GCCCTTCCTGCCTGCAATTGCTTCCAGTTGGTGGACGA  676

Qy   285  AspAsnValAlaGlyAlaProIleAsnGlyAlaHisIleGlyArgAsnGlyThrThrValLys  304
          |||                :::     |||
Db   677  AAACGCGATCGCAAGTTTCTGGATAAACGCGCTGGAAGAGTAC---CCGGACGCCCGCGAAA  733

Qy   305  TyrProValThrGlyAspValAlaAlaThrIleGlyUAsnIleLeuProHisValLysGlu  324
          |||        ::                   |||:||||
Db   734  GGGCTGCGACGATTTAGCTAAACCCGAGCCGAGAA------GCCATTCACCCGCGAAATTCTG  787
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 7900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 138:

US-08-956-171B-138

US-09-965-825-2 (1-579) x US-08-956-171B-138 (1-7900)

Alignment Scores:
Pred. No.:
Score: 790.50
Percent Similarity: 52.69%
Best Local Similarity: 32.80%
Query Match: 26.48%
DB:

Length: 7900
Matches: 183
Conservative: 111
Mismatches: 249
Indels: 16
Gaps: 8

RESULT 9
US-08-781-986A-138
; Sequence 138, Application US/08781986A

[Nucleotide/amino acid sequence alignment between Qy (query) and Db (database) rows follows, spanning the remainder of the page in two columns.]

Patent No. 6737248

GENERAL INFORMATION:

; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

; US-08-781-986A-138

Alignment Scores:
Pred. No.:
Score: 6.99e-77
Score: 790.50
Percent Similarity: 52.69%
Best Local Similarity: 32.80%
Query Match: 26.48%
DB: 4

Length: 7900
Matches: 183
Conservative: 111
Mismatches: 249
Indels: 16
Gaps: 8

US-09-965-825-2 (1-579) x US-08-781-986A-138 (1-7900)

Qy   7 GluGlnLeuIleAspThrLeuGlnGlnGlyValLysArgIleTyrGlyLeuValGly 26
            ||||: ||||:|| ||| ::|:
Db   1589 GAAGCATTAGTTAAAGCATTACAAGCATGGGATAAGATCACTTGTATTCCAGGA 1648

Db   1649 GACTCAAATCGACGC-ATAGTCGATAGTTACGTACAGTGAGAGATCAATTAAATTTTAT 1707
Qy   27 AspSerLeuAsnProIleValAspAlaValArg-----GlnSerAspIleGluTrpVal 44
            |||||| :|:   :::
Qy   45 HisValArgAsnGluGluValIleAlaAlaPheAlaAlaGlyAlaGluSerLeuThrGly 64
Db   1708 CATGTACGTCATGAAGAAGTAGCAAGCTTAGCGGCCTGCTGGTTACACAAAATTAACTGGT 1767

Qy   65 GluLeuAlaValCysAlaSerCysGlyProGlyAsnThrHisLeuIleGlyLeu 84
Db   1768 AAAATCGGTGTGGCAATTAAGTATCGGGTGGCCCTGGTTTAATTCATTTAATTAAATGGTATG 1827

Qy   85 TyrAspSerHisArgAsnGlyAlaLysValLeuAlaIleAlaSerHisIleProSerAla 104
Db   1828 TATGATGCCAAAAATGGATAATGTACCGGACAAACGAATAGTACA 1887

Qy   105 GlnIleGlySerThrPhePheGlnLThrHisProGluIleLeuPheLysGluCysSer 124
Db   1888 GCACTTGGAACGAAAGCAATCCAAGAAAAAATTTACAAAAATTATGTGAAGAATGTAGCC 1947

Qy   125 GlyTyrCysGluMetValAsnGlyGluGlnGlyGluArgIleLeuLeuHisHisAlaIle 144
Db   1948 GTTTAATAATCACCAAATTGAAAAGGTGACAAATGTGTTTGAAAATCGTTAACGAAGCAATT 2007

Qy   145 GlnSerThrMetAlaGlyLysGlyValSerValValValIleProGlyAspIleAlaLys 164
Db   2008 CGTACGGGCATATCGACAAAAAGGTGAGCGTTGTTGTTATTCCTAACGACTTTATTAACT 2067

Qy   165 GluAspLeuGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrPro---Val 183
Db   2068 GAAAAAATTAAAGATACAACG------AATAAACCAGTAGGATACATCAAGACCAACAGTA 2121

Qy   184 ValPheProAspProThrGluIleAlaAlaLeuValGluAlaIleLeuAsnAsnAlaLysSer 203
Db   2122 GTTATCACCAAAATATAAAGACATCAAAAAGCGGTTAAACTAATTAAAAAAGTAAAAAG 2181

Qy   204 ValThrLeuPheCysGlyValGlyAlaGlyValLysAsnAlaArgAlaGlnValLeuGluAla 223
Db   2182 CCTGTCATGTTAATTGGTGTAGGTGCGAAAACATGGAAAGATGAGCTACGTGAATTTAATT 2241

Qy   224 GluLysIleIleLysSerProIleGlyHisIleAlaLeuGlyLysGlnTyrIleGluHisGlu 243
Db   2242 GAAAATGGCTAAAAATTCCTGTCATTCATTCACTTACCAGCTAAAACAAATCTGCCGGACGAT 2301

Qy   244 AsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValAspAlaSer 263
Db   2302 CATCCATATAGTATCGGTAACTTAGGTAAAATCGGTAACAACATCTTTATCAAACATG 2361

Qy   264 AsnGluValAlaAspLeuAsnIleLeuLeuGlyThrAspPhePheProTyrSerAspPheLeuPro 283
Db   2362 CAGGAAGCGGATTTAATTAATTAATGGTTGGTACAACTAATCCATATGTGGATACTTACCT 2421

Qy   284 LysAspAsnVal------AlaGlnValAspIleLeuAsnGlyAlaHisIleGlyArgArgThr 301
Db   2422 AAGAAAAATATTAAAGCCATTCAAAATGACACAAATTCCTAAAAAATAACGGGACATCGTTTC 2481

Qy   302 ThrValLysTyrProValThrGlyAspValAlaLaAlaThrIleGluAsnIleLeuProHis 321
Db   2482 AATATTAAATGTAGGAAATTGTTGGAGATAGTAAAATTGCGTTGCATCAGTTAACTTGAAAAT 2541

Qy   322 ValLysGluLysThrAspArgSerPheLeuAsnAspArgMetLeuLysAlaHisGluArgLys 341
Db   2542 ATTAAACATGTTGCTGAAAGACCATTCTTAAACAAAAGGTTA-----GAAGCGTAAA 2592

Qy   342 Leu-------SerSerValValGluThrTyrThrHisAsnValGluLysHisSerValProIle 359
Db   2593 GCCGGTTTCGGATAAAATGGATGGAACAAGAATAAAAATATAATAAGTGTAAA------CCATTA 2646

Qy   360 HisProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspValAspAlaValPheThr 379
Db   2647 CGTCCAGAACGATTAAATGCATCAATCAAATAAATTTATTAAAGATGCAGTTGAATTCA 2706

Qy   380 ValAspThrGlyMetGlyMetCysAsnValTrpHisIleAlaArgTyrIleGluAsnProGluGlyThr 399
Db   2707 GCGAGATGTAGGTATGCAGCCAACAGTTTGGTCAACTCGATACTTA--AACCTTGGTGTGTAAAT 2763

Qy   400 ArgAspPhePheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIle 419
Db   2764 AACAAGTTCATCATTTCAAGTTGGTTAGGTACGAATGGGGTTGCGGTCTTCCAGGTGCAATT 2823

Qy   420 GlyAlaGlnSerValAspArgAsnArgGlnValIleLeuAlaMetCysGlyAspGlyGlyLeu 439
Db   2824 GCATCAAAAAATTGCATACATCCAAATAGACAAGCCAATTGCCTGGTCAGACGGTGCAATTC 2883

Qy   440 GlyMetLeuLeuGlyGluLeuLeuThrValLysGlyHisGlnLeuProLeuLysSerAlaVal 459
Db   2884 CAAATGGTAATGCAAGACTTCGCTACAGCAGTAACAATGATTACTTTAACTGTGATTT 2943

Qy   460 ValPheAsnAsnSerSerLeuGlyMetValLysGluGlnMetLeuValGluGlnGlnProPro 479
Db   2944 GTACTTAATAACAAACAGTTAGCATTTTTATTAATATTGAACACAGAAGCAGCTGGTTGAATTA 3003

Qy   480 GluPheGlyThrAspHisGlyGluValAsnPheAlaGluIleAlaAlaAlaAlaAlaGlyIle 499

RESULT 10

US-09-134-001C-1619

; Sequence 1619, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 1619

; LENGTH: 1761

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-1619

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

	2.19e-73	Length: 1761
	749.50	Matches: 172
	50.98%	Conservative: 114
	30.66%	Mismatches: 254
	25.11%	Indels: 21
	3	Gaps: 9

US-09-965-825-2 (1-579) x US-09-134-001C-1619 (1-1761)

```
Qy   497 AlaGlyIleLysSerValArgIleThrAspProLysLysValArgGlnGlnLeuLeuGlu 516
         ||||||        ::::::                           :::
Db  1510 GCTGGTGGTTAAAGGCTATGTTGTGAAAGATGTAAGTGCTGTCTTGACACATCGTTGAAGAG 1569

Qy   517 AlaLeuAlaTyrProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSer 536
         :::::::        ||||||                :::::::  ||||    ||
Db  1570 GCAATGGCTCAAGAAGTTCCAACAATCGTTGACGTTCAATGTTGATCCTAATGCTGCACCA 1629

Qy   537 IleProProThrIleThrTrpGluGlnValMetGlyPheSerLysAlaAlaAlaThrArgThr 556
         ::::||||         :::  |||||    :::    ||||    :::
Db  1630 TTACCAGGTAAAATTGTAAACGAAGAAGCATTTGGTTACAGTAAAATGGGCTTATAGATCA 1689

Qy   557 Val 557
         |||
Db  1690 ATT 1692
```

RESULT 11
US-09-252-991A-8458
Sequence 8458, Application US/09252991A
Patent No. 6551795
;
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8458
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8458

Alignment Scores:
Pred. No.:
Score: 1.49e-72   Length: 2577
Percent Similarity: 744.50   Matches: 191
Best Local Similarity: 51.85%   Conservative: 104
Query Match: 33.57%   Mismatches: 241
                         24.94%   Indels: 33
DB: 4   Gaps: 13

US-09-965-825-2 (1-579) x US-09-252-991A-8458 (1-2577)

Qy   1 MetAlaHisSerTyrAlaGlnGluGlnLeuIleAspThrLeuGluAlaGlnGlyValLysArg 20
         ||:||| ::: ||| ||||| | ||:| |:|::
Db   805 ATGGCCAGCAGCTACGCGCGGATCAATTGCTCGAACCCTTGAGCCAGTTGGGGGTAAGCGC 864

Qy   21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAlaAspAlaVal------ArgGln 38
         ::::::: ||| ::::::: |||| ||||
Db   865 GTCTTCGGGCTGGTACCAGGCGATCAACGGGATCGTGGCGGACGCCGTGGGGGGTAAGCGC 924

Qy   39 SerAspIleGluArgProValHisSerValArgAsnGlyGluAlaAlaAlaPheAlaAlaGlyAla 58
         ::::: || :::::: :::   :: ||||
Db   925 GAGGCATTCGAACTATATCCGGTGCGCCGACGAGATGGCCGCCTTCATGGCCGGCCGCGCC 984

Qy   59 GluSerLeuIleThrGlyLeuAlaValAlaCysAlaLeuSerCysGlyProGlyAsnThr 78
         ||:: ||| ::: |||||||| ||||
Db   985 CAGCGCAAGTTCACCGGACGGAGGTCGGCGGGTGTGGCCTCGGCGCCGGGGGGTAAGCGC 1044

Qy   79 HisLeuIleGlyLeuValTyrArgAspSerHisArgAsnGlyAlaLysValIleLeuAlaIleAla 98
         ||| ||| ::::::: |||| ::::::
Db 1045 CACCTGGTCGAAGCGGGCCTTACGACGCCGGTGCTGGCCATCGCGATCGTCGCCATCGTC 1104

Qy   99 SerHisIleProSerAlaGlnIleIleGlyLeuSerThrPhePheGlnGlnThrHisProGlnIle 118
         ::::::: |||| ::::::: |||| :::
Db 1105 GGCCAGCAGGCGGGCGCCTACGGCGTTGGGGCAGGACTACCAGCCGAAGAGTCGCGAGAGC 1164

Qy   119 LeuPheLysGluCysSerGlyLysTyrCysGluMetValAsnGlyValGlyGluArg 138
         |||:|| ::: ||| ||||| | ||:| |:|::
Db 1165 TTGTTCAAGGAGTGTTCCGGCTTAATGTGAGACCTGGTTCAGCCGCCCAGTTGCTCCAT 1224

Qy   139 IleLeuIleHisHisAlaIleGlnSerThrMetAlaGlyGlyValSerValValIle 158
         :::||| ::: ||| ||||| | ::::::
Db 1225 GTGCTGGACCGAGCCCTTGCCGGCGGTGGGCAGGTGCGACCGGTGATCGTG 1284

Qy   159 ProGlyValAspIleAlaLysGluGluAspAlaGlyAsp---GlyThrTyrSerAsnSerThrIle 177
         || ::::::: :::   :: |||
Db 1285 CCCAACGACGTGCAAGATGGCGCCCCGAAGCGCCCACGGCCACGTG 1344

Qy   178 SerGlyThrProValHisPheProAspPro---------ThrGluAla 191
         ::::::: ||| :::
Db 1345 AGTGGCGACGTGGGCTTCGTCCAGCCGCGAGGCGACGGCGACCTTGGAGGCC 1404

Qy   192 AlaAlaLeuValGlnAlaIleLeuAsnAsnAlaLysSerValThrLeuPheCysGlyValAlaGly 211
         ::: ||| :::   :::::::
Db 1405 GCCGCGCTGGTGCAGGCGATC-----CTCGAATCCGGCGGCGGCGGCGAGTCCTCGCGGGTCGCG 1458

Qy   212 ValLysAsnAlaArgAlaGlnValLeuLeuGluAlaGlyGluLysIleLeuSerProIleGly 231
         |||::: || :::::   :::::::
Db 1459 GCCCTGGGGCGCGGCACCGGCAACTGGAAGCGGGTGGGGGGGCGTCCCCCGAGTGGGC 1518

Qy   232 HisAlaAlaLeuValGlyGlyLysGlnThrTyrIleGluHisIleGlyAsnProGluGlyMetSer 251
         |||::: ||| ::: ||||
Db 1519 AAGGCGCTCCTGGTCGGCGGCAAGCAGACCTACGTTCCGCACATCGGCAACCCTGAGGGGCTC 1578

Qy   252 GlyLeuLeuGlyTyrGlyAlaCysValAspAlaSerAsnGluAlaAspLeuLeuIleLeu 271
         |||::: ||| :::::::
Db 1579 GGGCTGCTCGGGCACCCGCGCCCCAGCAACGGCGCATTGGCACACCCTGCTGATC 1638

Qy   272 LeuGlyThrArgPheProTyrSerAspPheLeuProLysValAspAsnAlaLeuAla------ 288
         |||::: ||| :::
Db 1639 GTCCGGCAGCACTTTCCCCTACGAGCAGTTCCTACCCAAGGTGGACAATGCGCTGGCG 1698

Qy   289 GlnValAspIleLeuAsnGlyValAlaHisSerIleGluGlyArgGlyThrThrValLysTyrProValThr 308
         ::::::: || :::::::
Db 1699 CAGATCGACCTGATCAACGGCGTATCCGCTATCCGGATCGACGGCCGTTGCTC 1758

Qy   309 GlyAspValAlaLeuAlaThrIleGluAsnIleLeuLeuProHisValLeuLysThrAspArg 328
         |||::: ||| :::::::
Db 1759 GGCGGATGCAGGGCGAAAACCCTGAGCGCGTCGCCGGCAGAGAAAAGCACGGC 1818

Qy   329 SerPheLeuAspArgMetLeuValAlaArgGlyLeuSerLeuSerValValGlnThr 348
         ::::::: ||| :::::::
Db 1819 GCCTGGCGCGCGCCGCGGGTC----------GAGCGGCGGGTGACGGCCAGTGCGGCGGAA 1866

Qy   349 TyrThrHisAsnValGlyLysHisVal---ProIleHisProGlyGlyTyrArgValAlaSerIle 367
         ::::::: ||| :::
Db 1867 GCCCGGCGCCGCCAGGCCGCGGAAGAGCCCAGCCGCACCCGAATCAACCCGAGCGGGGTATTCCGGTCC 1926

Qy   368 LeuAsnGlyLeuAlaAspLysAspArgLeuAlaValPheThrValAspTyrArgGlyMetCysAsnVal 387
         ::::::: ||| :::
Db 1927 TTGTCGGAGCAACTGCCGGACCGATGCAATGCATTCTCTGCGCGCAGCGGCGCTCCCATACCAAC 1986

Qy   388 TrpHisAlaArgTyrIleGluAsnProGluGlyThrArgAspPheValGlySerPhe--- 406
         |||::: |||
Db 1987 TGGTACCGCCGCCGCCAACGCCATGCCGCCCCGGGC----------ATGCTCGGCTCGGTCGTCG 2037

Qy   407 ---ArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleIleGluGlyValAlaGlnSerValAsp 425
         |||:::
Db 2038 GGCAAGCTGGGCGACCATGGGCGGCAGCGCGGCGCGGTGAACGCCGCCAGCGCGGGGTATTCCGGTAT 2097

Qy   426 ArgAsnArgGlnValIleAlaMetCysGlyValLeuGlyTyrMetLeu---LeuGly 444
         |||
Db 2098 CCGCAGCGCGCGGTTGGTGGCGGCGCTGCCGCGGGCGCCATGCAGATGAACGCCAACGCC 2157

Qy   445 GluLeuLeuThrValLysLeuHis--------------GlnLeuProLeuGlyLeuValVal 459
         |||
Db 2158 GAACTGGTCACCGTGCAGCAGTACTGGGACTGGGACTCGCGCGACCTTCATCGTGCTC 2217

Qy   460 ValPheAsnAsnSerLeuGlyMetValLysLeuGluMet---LeuValGluGlyGln 478
         |||
Db 2218 ...
```

RESULT 12
US-09-252-991A-8530

; Sequence 8530, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8530
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
;
DB: US-09-252-991A-8530

US-09-965-825-2 (1-579) x US-09-252-991A-8530 (1-2754)

Alignment Scores:

| Pred. No.: | 1.66e-72 | | Length: | 2754 |
|---|---|---|---|---|
| Score: | 744.50 | | Matches: | 191 |
| Percent Similarity: | 51.85% | | Conservative: | 104 |
| Best Local Similarity: | 33.57% | | Mismatches: | 241 |
| Query Match: | 24.94% | | Indels: | 33 |
| DB: | 4 | | Gaps: | 13 |

## Left column

Qy    460 ValPheAsnAsnSerLeuGlyMetValLysLeuGluMet---LeuValGluGlyGln 478
          ||||                 :::      |||||    ::
Db   2084 GTTCGAACAACGGCGATCTCAACCAGTGACCTGGGAGCACCGTGCCCTGCCCGAC 2143

Qy    479 ProGluPheGlyThrAspHisGlyLeuGluValAsnPhe------AlaGluIleAlaAlaAla 496
          ||||||                                      :::      |||
Db   2144 CCGGAGTTCAGCCCCGGGCCCCAGAAGTGATCATCGAATTCCCCTACGCCGCCATCGCCGCA 2203

Qy    497 AlaGlyIleLysSerValArgIleThrAspProLysValArgGluValLeuAlaGlu 516
          :::       |||                |||    ::
Db   2204 CTCGGCGTTCAAGGGACATCCGCCGGGATCGACGCCCGGCCTGGGGGCCGAG 2263

Qy    517 AlaLeuAlaThrTyrProGlyValLeuIleAspIleValThrAspProAsnAlaLeuSer 536
          :::                     ||||||
Db   2264 GCCTTCGCCCGGGTGCTGCTGGAGGTGGTCACCGACCCCGAACGTGCGGCCG 2323

Qy    537 IleProProThrIleThrThrTrpGluGln 545
          ||||||                  |||
Db   2324 CTGCCGGCCGCACATCAGTTTCCAGCAG 2350

RESULT 13
US-09-252-991A-7281/c
Sequence 7281, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
  APPLICANT: Marc J. Rubenfield et al.
  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
  FILE REFERENCE: 107196.136
  CURRENT APPLICATION NUMBER: US/09/252,991A
  CURRENT FILING DATE: 1999-02-18
  PRIOR APPLICATION NUMBER: 1998-02-18
  PRIOR FILING DATE: US 60/074,788
  PRIOR APPLICATION NUMBER: US 60/094,190
  PRIOR FILING DATE: 1998-07-27
  NUMBER OF SEQ ID NOS: 33142
  SEQ ID NO 7281
  LENGTH: 1113
  TYPE: DNA
  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7281

Alignment Scores:
  Pred. No.:
  Score:                   2.07e-67          Length:        1113
  Percent Similarity:      693.00            Matches:        142
  Best Local Similarity:   61.94%            Conservative:    81
  Query Match:             39.44%            Mismatches:     129
  DB:                      23.22%            Indels:           9
                                            Gaps:             4

US-09-965-825-2 (1-579) x US-09-252-991A-7281 (1-1113)

Qy      6 AlaGluGlnLeuIleAspThrLeuGluAlaGlnGlyValValLysArgIleTyrGlyLeuVal 25
          ||||                 ||||||               :::
Db   1059 GCCGAGATCGTCGTGGGAAACCCTGGAAGCGCCCGGGTCCGCCATTGCTATGGCATCGTC 1000

Qy     26 GlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAspIleGluTrpValHis 45
          |||       :::       ||                                   :::
Db    999 GGCGACACCCTCAACCATGTCACCGACGCCATCCGCGACGCCAGATCCAGTGGGTCCAC 940

Qy     46 ValArgAsnGlyGluAlaAlaAlaPheAlaAlaGlyValGluSerLeuIleThrGlyGlu 65
          :::                     |||||||||
Db    939 GTGCGCCACGAAGAGGCCGGCGGGCCTTCGCGGGACCGGGGTCGAGTCCCTGATCACCGGCGAG 880

Qy     66 LeuAlaValCysAlaLaAlaSerCysGlyTyrProGlyAsnThrHisLeuIleGlnTyrLeuTyr 85
          |||                     |||||||||
Db    879 CTGACCGCCGTGCGCGGCCGCCTGCGGGACCGGGAGTCCACTTCATCACGGCGGTCTAC 820

Qy     86 AspSerHisArgAsnGlyValLeuAlaLeuIleAlaSerHisIleProSerAlaGln 105
          :::::::                 ||       |||
Db    819 GAGGCCCAGCGCAACACCGGCGCAACCGGCCGATGTGCTGATCCCAGCCAGCAGATCGTTACCCGCCA 760

## Right column

Qy    106 IleGlySerThrPheGluGlnThrHisProGluThrLeuPheLysGluCysSerGly 125
          ||||                     :::       |||
Db    759 CTGGGCATGGAGTTTCCCACAGAGAGGTTCGATTCACAGGAGCACTTCAAGGAGTGCTCGGTG 700

Qy    126 TyrCysGlyMetValAsnGlyGluGlnGlyGlyValLeuGluHisHisAlaIleGln 145
          :::       |||       ::
Db    699 TTCTGCGGAGCAGGTGACGCAGACCCGGGGAACACGGCCGCGGGCCTCGCGCCAGCAG 640

Qy    146 SerThrMetAlaGlyLysGlyValSerValValValIleProGlyAspIleAlaLysGlu 165
          :::                     ||||||
Db    639 GCGGGCGTCAACCGGCGCCGGGGCCGTGGGCCGGGGTGGTGATCCTGCCCGGAGGCC 580

Qy    166 AspAlaGlyAspGlyThrTyrSerAsnSerGlyThrProValValPhe 185
          |||                     ||||||
Db    579 ACGGTGAAGGACGACCTG------CCGTTCTCGGGTGCATTTCCCCAGCC 526

Qy    186 ProAspProThrGluValAlaLeuAlaLeuAsnAsnAlaLysSerValThr 205
          |||                     :::
Db    525 CCCAGGCAGACCGGACTCAGGAGCGTCGCCCGGTCCCACGGGCAAGAGAATCGGC 466

Qy    206 LeuPheCysGlyAlaGlyValValLysAsnAlaArgAlaGlnValLeuGluLeuGluGlyLys 225
          ||||                     :::       :::
Db    465 ATCTACGCCGGCTCCGGTGCAGGGCGCCCACGACCTGCTGGGTGGCCCCTCGCCGACCGC 406

Qy    226 IleLeuSerProIleGlyTyrHisAlaLeuGlyGlyLysGlnLysTyrIleGlnHisHisGluAsnPro 245
          :::       |||
Db    405 CTCAGGCGCGCCATCGCGCACACGTCGCGGCGCAAGGACTTCGTGCGTACGACAACCC 346

Qy    246 PheGluValGlyMetSerGlyTyrLeuLeuGlyTyrGlyValAlaCysValAlaSerAsnGlu 265
          :::::::                 :::
Db    345 TTCAACATGGGCATGGCCGGTATCCTCGGCGATGCAGTGGCCTGCGTGGTGTCCAACGAG 286

Qy    266 AlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyrSerAspPheLeuPro---Lys 284
          :::                     |||
Db    285 TGCGACACCCTCCTCGTGCTCGGCGACTTCCCCGGGGCAGTTCTTATCCCAGAAG 226

Qy    285 AspAlaAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArgArgThrProValLys 304
          :::                     |||
Db    285 GCCAACGTGGCCCAGGTCGACATCAACGGCGCTCACCATCGGTCGGCGCACCCCATCGAT 166

Qy    305 TyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuProHisValGlu 324
          :::                     ::
Db    165 CTCCCGCCGGTCGGCGACGTG------ATCCC-CAGCTCTTGCCGTTGCGCCGAACC 116

Qy    325 LysThrAspArgSerPheLeuAspArgMetLeuLysAlaHisGluArgLysLysSerSer 344
          :::                     |||
Db    115 CGCCGAGGGACCGCAGCTTCCTCGACAGAATCGCCTGGACGACCGGAGGCTCGTGCGGACG 56

Qy    345 ValValGluThrTyrThrHisAsnValGlyLysHisValProIleHisProGluTyrVal 364
          :::       |||
Db     55 CTGGAAAAA------GAGGAGCAAGCCCGGCCAAGGGCGAGCTCGATCCATCGCGCACCTG 2

RESULT 14
US-09-252-991A-7413
Sequence 7413, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
  APPLICANT: Marc J. Rubenfield et al.
  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
  FILE REFERENCE: 107196.136
  CURRENT APPLICATION NUMBER: US/09/252,991A
  CURRENT FILING DATE: 1999-02-18
  PRIOR APPLICATION NUMBER: US 60/074,788
  PRIOR FILING DATE: 1998-02-18
  PRIOR APPLICATION NUMBER: US 60/094,190
  PRIOR FILING DATE: 1998-07-27
  NUMBER OF SEQ ID NOS: 33142
  SEQ ID NO 7413
  LENGTH: 1083
  TYPE: DNA
  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7413

Alignment Scores:
Pred. No.:
Score:      1.2e-66
Percent Similarity: 686.00
Best Local Similarity: 63.05%
Query Match:   40.47%
DB:       22.98%
        4

Length:   1083
Matches:  138
Conservative: 77
Mismatches: 120
Indels:   7
Gaps:    3

US-09-965-825-2 (1-579) x US-09-252-991A-7413 (1-1083)

```
Qy    6 AlaGluGlnLeuLeuIleAspThrLeuGluAlaGlnGlyValLysArgIleTyrGlyLeuVal   25
          |||||||
Db   43 GCCGAGAATCGTTCGTTGGAAAACCCTGGAAGCCCGGCCATTGTCTAGGCCATCGTC       102

Qy   26 GlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAspIleGluTrpValHis     45
Db  103 GGCGGACACCCTCAACCATGTCAACGACGCCGTCATCCATCGCAGCGACATCCAGTGGGTTCAC 162

Qy   46 ValArgAsnGluGluLeuAlaLeuAlaPheAlaLeuAlaGlyAlaGlyLeuSerLeuIleThrGlyGlu 65
Db  163 GTGCGCGCCACGAAGAACCGGCGGCCCTTCGCCCTGGCCCTGGCCGGCGCCGGCCTGAGCGC  222

Qy   66 LeuAlaValCysAlaAlaSerCysGlyProGlyValTyrAsnThrHisLeuIleGlnGlyLeuTyr 85
Db  223 CTGGCCGTCTGCGCCGCCTCCTGCGGACCGGGCGTCTACAACACGGGGTCTAC          282

Qy   86 AspSerHisArgAsnGlyValAlaLysValLeuAlaIleAlaSerHisIleProSerAlaGln  105
Db  283 GAGGCCCACCGGCGCCAACCCGGCGATGGTGCTACACGCCAGCATGCGTTACCCCCCAA     342

Qy  106 IleGlySerThrProPheGlnGluThrHisProGluIleLeuPheLysGluCysSerGly    125
Db  343 CTGGGCGCATGGAGAGTTCCCCAGGAGGTCGACTTCAAGCGGTTCGCTGCTCGGTG        402

Qy  126 TyrCysGluMetValAsnGlyValGlyGlnGlyLeuArgIleLeuHisSerAlaLeuGln    145
Db  403 TTCTCCGAGCAGGTGCACAGCCCGGAACAGGCGGGTGGTGGCCCTTGGCCTTGCCAG       462

Qy  146 SerThrMetAlaGlyValLysGlyValSerValValValIleProGlyAspIleAlaLysGlu 165
Db  463 GCGGCGCCTCAACCGGCCGCGGCCGTGGGCGTGATCCTGCCCGGCGACATCAGCCAGGCC    522

Qy  166 AspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrProValValPhe    185
Db  523 ACGGTGAAGCAGCGACCTG------CCGTTCTCGGTCATTTCCCGCAACCGGTGCTGCGC    576

Qy  186 ProAspProThrGluAlaLeuAlaLeuValGluAlaIleAlaAsnAlaLysSerValThr    205
Db  577 CCCAGCGACGCGGACGTGCACAGGGCGCTGCCCACGGCAGAGATCGGC               636

Qy  206 LeuPheCysGlyAlaGlyIleValLysAsnAlaArgAlaLeuGlnValLeuGluAlaGluLys 225
Db  637 ATCTACGCCGCCGGCTCCGGCTGCCCAGGCGCCCACGACCTGGTGGCCCTCGCCGACGGC    696

Qy  226 IleLeuSerProIleGlyHisIleAlaLeuLeuGlyLysGlnTyrIleGluGlnHisGluAsnPro 245
Db  697 CTCAAGGCGCCCATGCGCCACGTGCGGCCGGACACGGTACGACAACCC               756

Qy  246 PheGluValGlyMetSerGlyLeuLeuGlyTyrArgGlyValAlaCysValAlaSerAsnGlu 265
Db  757 TTCAACATGGGCATGAGCCGGTTATTGCTCGGATCGAGTCCCGGCTTCCACATGATGACCGAG 816

Qy  266 AlaAspLeuLeuIleLeuLeuGlyThrArgPheProTyrSerArgAspPheLeuPro---Lys 284
Db  817 TGCGACACCCTCCTGCTCGGGCCGGACTTCGCCTGGAGCCAGTTCTACCGGACACGAGAAG   876

Qy  285 AspAsnValAlaGlnValAspAspIleAsnGlyAlaHisIleGlyArgArgThrThrValLys  304
Db  877 GCCACCCTGATCCAGGTCGACCGGCGATGGAGCAGTCACCGACGAGGCATGGCCGTCGAT    936

Qy  305 TyrProValThrGlyAspValAlaAlaThrIleGluAsnIleLeuLeuProHisValLysGlu  324
```

```
Db  937 CTCGGCGGTGGTCGGCGACGTG--------ATCCC-CAGCTCTTGCCGTTGCTTCGAAGCC   986
Qy  325 LysThrArgAspArgSerPheLeuAspArgMetLeuLysAlaHisGluArgLysLeuSerSer  344
Db  987 CCGGAGGAGCGCAGCTTCCTCGACGAATGCCTGGGAGCACCGGCGAGCCGGAGCGGTCGGCGAGG 1046
Qy  345 Val 345
Db 1047 CTG 1049
```

RESULT 15
US-09-107-532A-3181
; Sequence 3181, Application US/0910752A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
  ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
  ADDRESSEE: GENOME THERAPEUTICS CORPORATION
  STREET: 100 Beaver Street
  CITY: Waltham
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02354
COMPUTER READABLE FORM:
  MEDIUM TYPE: CD/ROM ISO9660
  COMPUTER: PC
  OPERATING SYSTEM: <Unknown>
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/107,532A
  FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 60/085,598
  FILING DATE: 14 May 1998
  APPLICATION NUMBER: 60/051571
  FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: Ariniello, Pamela Deneke
  REGISTRATION NUMBER: 40,489
  REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (781) 893-5007
  TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3181:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1746 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: circular
  MOLECULE TYPE: DNA (genomic)
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  ORIGINAL SOURCE:
  ORGANISM: Enterococcus faecium
  FEATURE:
    NAME/KEY: misc_feature
    LOCATION: 1...1746
  SEQUENCE DESCRIPTION: SEQ ID NO: 3181:
US-09-107-532A-3181

Alignment Scores:
Pred. No.:
Score: 1.66e-61
Percent Similarity: 643.00
Best Local Similarity: 49.55%
Query Match: 28.55%
DB: 21.54%
        4

Length: 1746
Matches: 159
Conservative: 117
Mismatches: 259
Indels: 22
Gaps: 9

US-09-965-825-2 (1-579) x US-09-107-532A-3181 (1-1746)

```
Qy    9  LeuIleAspThrLeuGluAlaGlnGlyValLysArgIleTyrGlyLeuValGlyAspSer   28
            |||                    :::
Db   43  ATGGTAAAAGTTCTTGAAAAGTTACGGCTAATCACCATAATTACCGGCGATTCCCGAGGAATCT  102

Qy   29  LeuAsnProLeuValAspAlaValAlaArgGln------SerAspArgIleGluTrpValHisVal   46
            |||      ||| :::                     :::
Db  103  TTCAAATCAATTAATGGATGCCTATATCAACAGAAAAACCGAAATCAACTACATTCAAGTT  162

Qy   47  ArgAsnGluGluAlaAlaAlaPheAlaAlaGlyAlaGluSerLeuIleIleThrGlyGluLeu   66
            |||||||                 :::
Db  163  CGTCATGAAGGAAGTCGGCCACTCGCGAGCCCGCTGCGAGTGCAAAAATTAACGGGGAAAGTC  222

Qy   67  AlaValGlyAlaAlaSerCysGlyProGlyAsnThrHisLeuIleGlnGlyLeuTyrAsp   86
           |||||||        |||||||              ||||||      |||
Db  223  GGGCGCTGTTCGGGCTTCTGCAGGACCTGGCGCAGACATTTGATCAATGGTTTGTAATGAT  282

Qy   87  SerHisArgAsnGlyIleAlaLysValLeuAlaIleAlaSerHisIleProSerAlaGlnIle  106
           :::||||||          |||:::::::|||
Db  283  GCACAGATAGGACCATGTGCCCTCTAGTAGGTGTTGCTTTGCTTCTCACATCCATG  342

Qy  107  GlySerThrPhePheGlnGluThrHisProGluIleLeuPheLysGluCysSerGlyTyr  126
           |||                ||| :::      |||
Db  343  AACTATAACTCTTTCAGGAACTAAAATGAAAAATCCTATTTTCGCAGATGTTAGCGTATAC  402

Qy  127  CysGluMetValAsnGlyValGlyGluGlnGlyIleLeuLeuHisHisAlaIleGlnSer  146
           |||                ::: |||||||
Db  403  AATCGTACAGTCATGACACCAACAAAGTTCTTCCGCATGTAGTAGATGAAGCCCATTAAAGCC  462

Qy  147  ThrMetAlaGlyLysGlyValSerValValValIleProGlyAspIleAlaLysGluAsp  166
           |||||||   |||||||:::
Db  463  GCCTATGAGCATAAAGGCGGTGCTATCGTGTCATCCCTGTTGATCTTGGTTTTCGAAGAA  522

Qy  167  AlaGlyIleAspGlyThrTyrSerArgAsnThrIleSerSerGlyThrProValValPhePro  186
           |||||||              :::
Db  523  ATTGACGAACAACCTTTCTCCACGCGTCAC---ACTCACAAAACAAAGTGTGATTATTACCA  579

Qy  187  AspProThrGluAlaAlaAlaLeuValGluIleAlaAsnAsnAlaLysSerValThrLeu  206
           |||                ::: |||
Db  580  GAAGAAAAAAGATTTGCTAGCTGCTTTATCTTGAAAAAAGCAAAAAAACCAGTTCTT  639

Qy  207  PheCysGlyAlaGlyValLysAsnAlaLeuAlaArgAlaGlnValIleLeuGluHisHisAlaGlnSer  226
           |||:::|||        |||:::
Db  640  TATGTTGGTGCAAGGAACGCGAAACGGAATTCCGCAAATCAAAGAATTATGAAGACATTT  699

Qy  227  LysSerProIleGlyHisAlaLeuGlyGlyGlnThrTyrIleGluGlnHisGluAsnProPhe  246
           |||||||         |||:::
Db  700  TCAGTTCCTCGTTGTCGCTTCCGGTTCTAGCAAAGGAATTTATTCCTGATGATTATGAAAAC  759

Qy  247  GluValGlyMetSerGlyLeuLeuGlyTyrCysGlyAlaCysValAlaAspAlaSerAsnGluAla  266
           :::|||||||       |||:::
Db  760  TTTCTTGGTTTGCTGGAGTGTGCTACTAAACCCGGAAAATGAAGCAATGAAGAAGCC  819

Qy  267  AspLeuLeuIleLeuLeuGlyThrArgPheLeuLysTyr------SerAspPheLeuProLys  284
           |||||||||||:::::::|||||||             :::
Db  820  GATCTGATCTATTTTGTCCGTGATCGTTACCTTAGCGAATTCCTCGATTTTCAACCAACT  879

Qy  285  AspAsnValAlaGlnValAspIleAsnGlyAlaHisIleGlyArgTyrThrArgValLys  304
           |||||||   |||||||:::
Db  880  GCTGAATTTTATCCAAATCGATAATCGGTCGCTACTAAAATTTGGACGCCATGAAACATCT  939

Qy  305  TyrProValThrGlyAspArgValThrAspMetThrIleGluLeuLeuProHisIleValLysGlu  324
           |||      |||||||:::
Db  940  TTGTCGATCCTCCGTGATCGAAGGACTTGCAAAGACTTGTC  987

Qy  325  LysThrAspArgSerPheLeuAspArgMetLeuLysTyrAlaHisGlu------ArgLys  341
           |||                :::|||      |||
Db  988  TTAGGGGATGCTCCCCCTGCTGATGGCAAATCGGTACCTAGCGAAATCAAGAAAAAA  1047

Qy  342  LeuSerSerValValGluThrTyrThrHisSerAsnValGluIleProIleHisPro  361
           :::|||||||      :::
Db 1048  TGGGTAAAATTGGTTGAAAATCTTTTGAAGATCGAGCAGGAGAA------CCGATTCGTTCCA  1101

Qy  362  GluTyrValAlaSerIleLeuAsnGluLeuValLeuAspProLysAspAlaValPheThrValAsp  381
```

```
Db 1102  GAGGCTGTCTATATAAAGAAATCAAATCGTTAATTGCTGAAGACGATTTTTGCTCACAGAT  1161
              |||          :::|||

Qy  382  ThrGlyMetCysAsnValThrTrpHisSerAlaArgTyrIleGluAsnProGluGlyThrArgAsp  401
              :::
Db 1162  GTCGGTAACACGACTATC---CATTCTATTCGTTTATTGAATATGAACGGTTAAACAAAA  1218

Qy  402  PheValGlySerPheArgHisSerGlyThrMetAlaAsnAlaLeuProHisLeuAlaIleIleGlyAla  421
              |||           |||
Db 1219  CATACGACACTCTGGATGGGTTCGCCACTATGGGTAAGGGTGTGCCACAGGAGAATTGCCGCA  1278

Qy  422  GlnSerValAspArgAsnArgGlnValIleIleAlaIleAlaMetCysGlyAspGlyValGluGlyMet  441
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Db 1279  CAACTAAGCTACCCAGAAAAACAAGTAGTATTTACCTTAAGTGGTGTCTGATTGGTCTATG  1338

Qy  442  LeuLeuGlyGluLeuThrValLysGlnValLeuHisGluHisLeuProLeuHisSerAlaLeuValPhe  461
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Db 1339  GTCATGGCAAGATAATCAATTACACAACGTCAAAAATACCAGCTTCCAAATTATTAAAGTTGTCTTT  1398

Qy  462  AsnAsnSerSerLeuGlyMetValLysLeuGluLeuMetLeuValGlyLysGlyGlnProGluPhe  481
              |||           |||
Db 1399  TCGAATGAATCTTTTGGTTTCATCGAAAGCAGAACAAGAAGATGACACGGAACAAAAAGAAAATTT  1458

Qy  482  GlyThrAspHisSerGluGluValAlaAsnPheGluLeuIleLeuAlaAlaAlaLeuGlyIleLeuSer  501
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Db 1459  GGTGTATTTTTTAGATGAGAATGCGAAAGTTGGAGAAGCGCTCGGGGGCAAATAGC  1518

Qy  502  ValArgIleThrArgProLysGlyValAlaArgGluGlnLeuLeuAlaLeuAlaThrTyrPro  521
              |||                 :::
Db 1519  TTTACAGTCACAGAATAACTCCGCAACTTCGATTTGCCTTTGAGATAGCTGCAAAATCAGAT  1578

Qy  522  GlyProValLeuGluLeuAspIle------ValThrAspProAsnAlaLeuSerIle  537
              |||||||           :::
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Qy  538  ------ProProThrIleThrTrpGluGlnValMetGlyPheSerLys  551
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Db 1639  CATTTAGATCCAAGAAAAATATTCTCGAAGAAGAATCCAAGCCATTCAAAAGAA  1689
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: January 15, 2005, 14:12:37 ; Search time 880 seconds
(without alignments)
3780.533 Million cell updates/sec

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Perfect score: 2985
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Scoring table: BLOSUM62
Searched: 4300275 seqs, 2872944193 residues

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	Ygapop 10.0 ,	Ygapext 0.5
	Fgapop 6.0 ,	Fgapext 7.0
	Delop 6.0 ,	Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=200000000 -USER=US09965825 @CGN 1 1.627 @runat_14012005_093023_10355
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Match Length	DB ID	Description
1	2985	100.0	1737	17	US-09-738-626-2873	Sequence 2873, Ap
2	2985	100.0	1860	9	US-10-781-014-85	Sequence 85, Appl
3	2985	100.0	2160	9	US-09-965-825-1	Sequence 1, Appli
4	2985	100.0	2160	15	US-10-143-856-3	Sequence 3, Appl
5	2985	100.0	2160	15	US-10-078-167-4	Sequence 4, Appli
6	2985	100.0	2160	15	US-10-336-049-4	Sequence 4, Appli
7	2985	100.0	2160	15	US-10-091-342-4	Sequence 4, Appli
8	2985	100.0	2160	16	US-10-686-736-4	Sequence 4, Appli
9	2985	100.0	3248	9	US-09-965-825-4	Sequence 4, Appli
c 10	2985	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 11	2300.5	77.1	1734	15	US-10-282-122A-17635	Sequence 17635, A
12	1746	58.5	1740	15	US-10-156-761-2067	Sequence 2067, Ap
c 13	1746	58.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
14	1590	53.3	944	17	US-10-781-014-89	Sequence 89, Appl
15	1518	50.9	875	9	US-09-965-825-3	Sequence 3, Appl
16	1518	50.9	875	15	US-10-143-856-5	Sequence 5, Appli
17	1518	50.9	875	15	US-10-078-167-5	Sequence 5, Appli
18	1518	50.9	875	15	US-10-336-049-6	Sequence 6, Appli
19	1518	50.9	875	15	US-10-091-342-6	Sequence 6, Appli
20	1518	50.9	875	16	US-10-686-736-6	Sequence 6, Appli
21	1367	45.8	1716	16	US-09-738-626-1	Sequence 6, Appli
22	1338	44.8	1722	16	US-10-282-122A-33768	Sequence 33768, A
23	1336	44.8	1722	16	US-10-282-122A-32583	Sequence 32583, A
24	1317.5	44.1	1719	16	US-10-282-122A-41795	Sequence 41795, A
c 25	1317.5	44.1	1719	9	US-09-815-242-6012	Sequence 6012, Ap
26	1317.5	44.1	1719	14	US-10-096-571-1	Sequence 1, Appli
27	1317.5	44.1	1719	16	US-10-282-122A-20313	Sequence 20313, A
28	1316.5	44.1	1737	16	US-10-282-122A-12285	Sequence 12285, A
29	1309.5	43.9	1716	16	US-10-282-122A-23384	Sequence 23384, A
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31	1298.5	43.5	1719	9	US-09-815-242-9898	Sequence 9898, Ap
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33	1284	43.0	1728	16	US-10-282-122A-14452	Sequence 14452, A
34	1249.5	41.9	1710	15	US-10-369-493-39295	Sequence 39295, A
35	1249.5	41.9	1710	15	US-10-369-493-39670	Sequence 39670, A
36	1249.5	41.9	1710	15	US-10-369-493-40028	Sequence 40028, A
37	1243	41.6	1806	16	US-10-282-122A-13519	Sequence 13519, A
38	1239	41.5	1725	15	US-10-369-493-34030	Sequence 34030, A
39	1222	40.9	1767	16	US-10-282-122A-11945	Sequence 11945, A
40	1166	39.1	1761	9	US-09-738-626-1	Sequence 943, App
41	1166	39.1	9025608	15	US-10-156-761-1	Sequence 1, Appli
42	1101	36.9	1719	16	US-10-282-122A-30639	Sequence 30639, A
43	990.5	33.2	1448	13	US-10-096-571-8	Sequence 8, Appli
44	927	31.1	1454	13	US-10-096-571-7	Sequence 7, Appli
45	927	31.1	1454	14	US-10-076-416-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-738-626-2873

; Sequence 2873, Application US/09738626
; Sequence 2873, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US2002019760SA1
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16

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;   PRIOR APPLICATION NUMBER: JP 00/159162
;   PRIOR FILING DATE: 2000-04-07
;   PRIOR APPLICATION NUMBER: JP 00/280988
;   PRIOR FILING DATE: 2000-08-03
;   SOFTWARE: PatentIn ver. 3.0
;   NUMBER OF SEQ ID NOS: 7059
;   SEQ ID NO 2873
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-2873

Alignment Scores:
Pred. No.:
Score:                    1.71e-272
Score:                    2985.00
Percent Similarity:       100.00%
Best Local Similarity:    100.00%
Query Match:              100.00%
DB:                       9

US-09-965-825-2 (1-579) x US-09-738-626-2873 (1-1737)

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                          Conservative:     0
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Qy   61 LeuIleThrGlyGlyLeuLeuAlaValCysSerAlaAlaSerCysGlyPro...   80
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Qy  141 HisHisAlaIleGlnSerThrMetAlaGlyIleLysSerGlyValValVal...  160
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Qy  201 AlaLysSerValThrLeuPheProSerGlyTyrHisAlaLeuGlyHisAla...  220
   601 GCTAAGTCTGTCACTTTGTTCCCGGGATCGGGCAGATGAAGTGCTGGG       660

Qy  221 GluLeuAlaLeuAspLysLysSerProIleGlyLeuValGlyGlnTyrIle  240
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Qy  241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuTyrGlyValCys... 260
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Qy  261 AspAlaSerAsnGlnAlaAspLeuLeuLeuLeuGlyThrAspAspAspPhe... 280
   781 GATGCGGTCCAATCGAGGCCGGATCTGCTGCTTGATTCTTATTCTGAT      840

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Qy  341 LysLeuSerSerValValGluThrArgThrHisAsnValGluGlyValPro...  360
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Qy  361 ProGluThrValValAlaSerIleLeuAsnGluLeuAlaAspGlyAsnAsp... 380
  1081 CCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCCGGATCAAGAGATG   1140

Qy  381 AspThrArgGlyMetCysAsnValThrTrpHisAlaArgThrIleGluLeu... 400
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;  APPLICANT:   Zelder, Oskar
;  APPLICANT:   Haberhauer, Gregor
;  TITLE OF INVENTION:  CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN CARBON METABOLISM AND ENERGY
;  TITLE OF INVENTION:  PRODUCTION
;  FILE REFERENCE:  BGI-126CPCN
;  CURRENT APPLICATION NUMBER:  US/10/781,014
;  CURRENT FILING DATE:  2004-02-17
;  PRIOR APPLICATION NUMBER:  US 09/602,740
;  PRIOR FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER:  60/141,031
;  PRIOR FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER:  60/143,208
;  PRIOR FILING DATE:  1999-07-09
;  PRIOR APPLICATION NUMBER:  60/151,572
;  PRIOR FILING DATE:  1999-08-31
;  PRIOR APPLICATION NUMBER:  DE 19931412.8
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931413.6
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931419.5
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931420.9
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931421.7
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931424.1
;  PRIOR FILING DATE:  1999-07-08
;  PRIOR APPLICATION NUMBER:  DE 19931428.4
;  PRIOR FILING DATE:  1999-07-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 784
;  SEQ ID NO 85
;  LENGTH: 1860
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (101)..(1837)
;  OTHER INFORMATION: RXN000635
US-10-781-014-85

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Score:                2985.00
Percent Similarity:   100.00%
Best Local Similarity: 100.00%
Query Match:          17

Matches:      579
Conservative: 0
Mismatches:   0
Indels:       0
Gaps:         0

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RESULT 3
US-09-965-825-1

Sequence 1, Application US/09965825
Patent No. US20020150999A1
GENERAL INFORMATION:
  APPLICANT: DUSCH, Nicole
  APPLICANT: THOMAS, Hermann
  APPLICANT: THIERBACH, Georg
  TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID U
  TITLE OF INVENTION: CORYNEFORM BACTERIA
  FILE REFERENCE: 21354US0X
  CURRENT APPLICATION NUMBER: US/09/965,825
  CURRENT FILING DATE: 2001-10-01
  PRIOR APPLICATION NUMBER: DE 10048604.5
  PRIOR FILING DATE: 2000-09-30
  PRIOR APPLICATION NUMBER: DE 10117085.8
  PRIOR FILING DATE: 2001-04-06
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn version 3.1

SEQ ID NO 1
  LENGTH: 2160
  TYPE: DNA
  ORGANISM: Corynebacterium glutamicum
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (327)..(2063)
  OTHER INFORMATION:
  NAME/KEY: -35_signal
  LOCATION: (227)..(232)
  OTHER INFORMATION:
  NAME/KEY: -10_signal
  LOCATION: (256)..(261)
  OTHER INFORMATION:

US-09-965-825-1

Alignment Scores:
Pred. No.:
Score:                          2985.00
Percent Similarity:             100.00%
Best Local Similarity:          100.00%
Query Match:                    9

DB:                             2.28e-272

US-09-965-825-2 (1-579) x US-09-965-825-1 (1-2160)

Length:            2160
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Mismatches:           0
Indels:               0
Gaps:                 0
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Db  447  ATTGAGTTGGGGTGCACGTTCGAAATGAGGAAGGAGGAGCCGGTTGCAGCCGGGGATCG     506

Qy   61  LeuIleLeuThrGlyGluLeuAlaValCysAlaAlaSerCysGlyLysProGlyAsnThrHisLeu  80
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Db  507  TTGATACTCGGGGAGCTGGCAGTATGTGCTGCTTCTTGTGGTCCTGGAAAACACACCTG     566

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Db  567  ATTCAGGGTCTTTATCGTGATTCCCATCGAAATGGTGCCGCCGTTCTTGCTATCGCCCAT  626

Qy  101  IleProSerAlaGlnIleLeuSerThrArgPhePheGluGlnIleLeuGluPhe          120
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Db  627  ATTCCGAGTGCCCAGATTCTTTCCACGAGATTCTTCGAAGAGATTTTGGAGTTC         686

Qy  121  LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGlyGlnGlyGluArgIleLeu    140
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Db  687  AAGGAATGCTCGGGTTACTGCGAGATGGTGAATGGTGGTGGGCAGGGTGAACGCAATTTG   746

Qy  141  HisHisAlaIleLeuGlnSerThrMetAlaGlyLeuGlyLysGluValSerValValIlePro  160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  747  CATCACGCGATTCAGTCCACCATGGCCGGCTGTAAAGGTGTTCGGGTGGTAGTTCCTGGT   806

Qy  161  AspIleAlaLysGluAspAlaAlaGlyLysGlyTyrThrTyrSerAsnSerThrIleSerSerGly  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  807  GATATCGCTAAGGAAGACGCAGGTGGACGGCTACTTAATTCCAATTCCACTATTCTTGGC   866

Qy  181  ThrProValPheProAspProThrGluValAlaAlaAlaLeuValGluAlaLeuAlaAsnAsn  200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  867  ACTCCTGTGTTTCCGGATCCTACTGAGGTCGCAGCCGCTTTGGTGGAGGCGCTTAACAAC  926

Qy  201  AlaLysSerValThrLeuPheCysGlyAlaAlaGlyValAlaGlyValValLysSerAsnAlaAlaArgAlaGlnAlaGlnGluValVal  220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  927  GCTAAGTCTGTCACTTTGTTCTGCGGTGCCGGTGTAGCAGGTGTTGTCAAGAGCAATGCTGCAAGAGCTCAGGCTCAGGAAGTTGTG  986

Qy  221  GluLeuValAlaGluLysIleIleLysSerSerProIleGlyHisAlaLeuGluGlyLysGlnTyrIle  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  987  GAGTTGGTCGCGGAGAAGATTATAAAATCACCGATCGGGCATGCGCTGGAAGGCAAGCAGTACATC  1046

Qy  241  GlnHisGlyAsnProPheGluValGlyMetSerGlyTyrLeuLeuGlyTyrGlyAlaCysVal     260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1047 CAGCATGGAAATCCGTTTGAGGTCGGCATGTCTGGGTTACGGCGTGCGTG               1106

Qy  261  AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrArgPhePheProTyrSerAsp      280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1107 GATGCCGTCCAATGAGGCGGATCTGCTAATCTTGCTTGGAACACGCTTCTTTCCTTATTCTGAT    1166

Qy  281  PheLeuProLysAspAspAsnValAlaGlnIleValAspIleAsnGlyValAlaHisIleGlyArgArg  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1167 TTCCTTCCTAAAGACAACGTTGCCCAGATCGTTGATATCAACGGTGTCGCACATATTGGTCGACGT  1226

Qy  301  ThrThrHisValLysTyrProValThrArgGlyAspValAlaAlaThrIleGluAsnIleLeuAsnPro  320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1227 ACCACGGTGAAGTACCCGGTGACCCGTGGTGACGTCGCAGCAACTATCGAAAATATTTTGCCT     1286

Qy  321  HisValLysGlyLysThrAspArgSerPheLeuValAlaSerAlaHisGluArg          340
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1287 CATGTTAAAGGGAAAACAGATCGTTCCTTCCTCGTTGCTTCGGCTCACGAGCGT          1346

Qy  341  LysLeuSerSerValAlaGluThrTyrThrHisAsnAspValGlyLysHisValProIleHis  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1347 AAGTTGAGCTCGGTTGCTGAAACGTACACACACAACGATGTCGGAAAGCATGTTCCGATTCAC   1406

Qy  361  ProGluTyrValAlaSerIleLeuAspAsnGluLeuAlaGlyLysAspAlaValPheThrVal  380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1407 CCTGAATACGTTGCCTCTATTTTGGATAACGAGCTGGCCGGCAAGGATGCCGTGTTTACTGTG   1466

Qy  381  AspThrGlyMetCysAsnValTrpHisArgTyrIleGluAsnProGlyThrArg         400
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1467 GATACGGGCATGTGCAATGTGTGGCATCGGTACATCGAGAATCCGGGAACGCGG          1526

Qy  401  AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly    420
Db  1527 ...                                                             1586
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Qy  481  PheGlyThrAspHisGlyLeuGluValAsnPheLeuAlaGlyIleIleAlaAlaAlaGlyIleIleLys  500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1541 TTTGGTACTGACCATGAGGGAAGTGAATTTCCGAGAGATTGGCGGCGGCTGCGGGTATCAAA   1600

Qy  501  SerValArgIleThrAspProLysArgGluGlnLeuLeuAlaGlyIleAlaLeuAlaAlaTyr  520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1601 TCGGTACGCAATCACCGGATCCGAAGAAAGTTCGGACGAGCAGTTAGCTCGATAT          1660

Qy  521  ProGlyProValLeuIleAspIleValThrAspProAsnAlaAlaLeuSerIleProProThr  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1661 CCTGGACCTGTTACTGGATATCGTTCACGGATCCAACGCCGCCACCA                 1720

Qy  541  IleThrTrpGluGlnValValMetGlyPheSerLysLysValAlaAlaThrArgThrValPheGlyGly  560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1721 ATCACGTGGGAACAGGTCATGGGATTCAGCAAGAAGGGCAACCGGGAAGTT             1780

Qy  561  GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro       579
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1781 GGAGTAGGAGCGGATGATCGACATAAGGAAATATTCCTACTCCA                    1837
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RESULT 4
US-10-143-856-3

Sequence 3, Application US/10143856
Publication No. US20030109014A1
GENERAL INFORMATION:
  APPLICANT: BURKE, KEVIN
  APPLICANT: DUNICAN, L.K.
  APPLICANT: McCORMACK, ASHLING
  APPLICANT: STAPLETON, CLIONA
  APPLICANT: MOCKEL, BETTINA
  APPLICANT: THIERBACH, GEORG
  TITLE OF INVENTION: Process for the fermentative preparation of
  TITLE OF INVENTION: L-amino acids
  TITLE OF INVENTION: with amplification of the tkt gene
  FILE REFERENCE: MAS//021123/282432
  CURRENT APPLICATION NUMBER: US/10/143,856
  CURRENT FILING DATE: 2002-05-14
  PRIOR APPLICATION NUMBER: 09/986,649
  PRIOR FILING DATE: 17-03-2000
  NUMBER OF SEQ ID NOS: 12
  SOFTWARE: Patentin Ver. 2.1
  SEQ ID NO 3
  LENGTH: 2160
  TYPE: DNA
  ORGANISM: Corynebacterium glutamicum
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (327)..(2063)
  OTHER INFORMATION: poxB
US-10-143-856-3

Alignment Scores:
  Pred. No.:
  Score:                     2.28e-272
  Percent Similarity:        2985.00
  Best Local Similarity:     100.00%
  Query Match:               100.00%
                             100.00%
                             15

  Length:        2160
  Matches:       579
  Conservative:  0
  Mismatches:    0
  Indels:        0
  Gaps:          0
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RESULT 5
US-10-078-167-4
Sequence 4, Application US/10078167
Publication No. US20030119154A1

GENERAL INFORMATION:

; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Ciona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 99029 BI-US-B
; CURRENT APPLICATION NUMBER: US/10/078,167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB

US-10-078-167-4

Alignment Scores:

Pred. No.:
Score: 2.28e-272   Length: 2160
Percent Similarity: 2985.00   Matches: 579
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
                             100.00%   Indels: 0
DB: 15   Gaps: 0

US-09-965-825-2 (1-579) x US-10-078-167-4 (1-2160)

Qy   1 MetAlaHisSerTyrAlaGluGlnLeuLeuIleAspThrLeuGluAlaGlnGlyValLysArg 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 327 ATGGCACACAGCTACGCCGAGCAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 386

Qy   21 IleLeuThrGlyTyrValGlyTyrAspAspSerLeuAsnProIleValAlaValAlaGlnSerAsp 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 387 ATTTTAACTGGTTATGTGGGCTATGACGATTCCTTAAATCCGATCGTTGCAGTCGCCCAATCAGAT 446

Qy   41 IleGluTrpValHisValArgAsnGluGluAlaAlaLeuGlyAlaAlaGlyAlaGluSer 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 447 ATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCTTTGGGTGCGGCAGGTGCGGAATCG 506

Qy   61 LeuLeuThrGlyValGluLeuAlaValAlaSerCysGlyProGlyAsnThrHisLeu 80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 507 TTGATCACTGGCGGAGCTGGCCAGTAGTGTCGCGTTCTTCTTGTGGTCCTCGGAAACACACCTG 565

Qy   81 IleGlnGlyLeuTyrAspSerHisArgAsnGlyAlaLysLeuAlaLeuAlaSerHis 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 567 ATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCAAAGTCGGCACTGGCCTCTAGCCAT 626

Qy 101 IleProSerAlaGlnIleIleGlySerThrPheGlnGluThrHisProGluIleLeuPhe 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 627 ATTCCGAGTGCCCAGATTATTGGTTCGACGTTCCAGGAAACGCATCCGGAGATTTTGTTT 686

Qy 121 LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGluGlnGlyGlyArgIleLeu 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 687 AAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGTGAGCAGGGTGGAGCATTTTG 746

Qy 141 IleThrTrpGluGlnValMetGlyPheSerIleLysValSerValValIleProGly 160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 747 ATCACGTGGGAACAGGTCATGGGATTCAGCAAGGTGTCGGTGGTAGTGATTCCTGGT 806

Qy 161 AspIleAlaLysGluAspAlaLysGlyAspGlyTyrThrTyrSerAsnSerGlyGly 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 807 GATATCGCTAAAGAAGACGCAAAAGGTGACGGGTACTTATTTATTCCACTATTTCTGGC 866

Qy 181 ThrProValValPheProAspProThrGluAlaIleAlaAlaLeuAlaGluAlaIleAlaAsnAsn 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 867 ACTCCTGTGGTTGTTCCCGGATCCTACTGAGGCCATCGCTGCCCTGGCTGAGGCAGGATTAACAAC 926

Qy 201 AlaLeuLysSerValThrLeuProPheCysGlyIleAlaGlyTyrAsnAlaArgAlaGlnValLeu 220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 927 GCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTTAGAAGAATGCTCGGCAGGTGTTG 986

Qy 221 GluLeuAlaGluLysIleLysSerProIleGluGlyHisIleAlaLeuGlyGlyLysTyrIle 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 987 GAGTTGGCCGAGAAGATTAAATCACCGATCGAGGGCCACATCGCGCTGGGTGGGCAGTACATC 1046

Qy 241 GlnHisGluAsnProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysVal 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1047 CAGCATGAGAATCCGTTTGAGGTCGGCATGTCTGGTCTGCTTGGTTACGGCGCCTGCGTG 1106

Qy 261 AspAlaLysSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrArgPheGluProTyrSerAsp 280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1107 GATGCGTCCAATGAGCGGGATCTGCTGATTCTATTGGGTACGCGGATTCCCTTTATCTGAT 1166

Qy 281 PheLeuProLysAspAsnValLeuAspIleAlaHisIleGlyTyrArgArg 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1167 TTCCTTCCTAAAGACAACGTTCTGGACATCGCCCACATCGGATATCGACGT 1226

Qy 301 ThrThrValLysTyrProValThrGlyAspValAlaAlaAlaThrIleGluIleLeuPro 320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1227 ACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCAGCAAATCGAAAATATTTTGCCT 1286

Qy 361 ProGluTyrValAlaLeuSerIleLeuAsnGluLeuAlaAspLysSerAspAlaValPheThrThrVal 380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1407 CCTGAATACGTTGCCTCTATTTGAACGAGCTAGCTCGCCGGATAAGACGCGTGTTTACTGTG 1466

Qy 381 AspThrGlyMetCysAsnValTrpHisSerLeuArgTyrIleGluLeuAsnProGluGlyThrArg 400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1467 GATACCGGCATGTGCAATGTGTGGCATAGCCGAGGTTACATCGAGGTACTGAATCCGGAACGCGGC 1526

Qy 401 AspPheValAlaGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1527 GACTTTGTGGGGTTCATTCGGCACGGTACCATGGCTAATGCCCTGCCTCATGCCATTGGT 1586

Qy 421 AlaGlnSerValAspAlaArgAsnArgGlnValIleIleAlaMetCysGlyAspGlyGlyTyrGlyLeuGly 440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1587 GCGCAAAGTGTTGATGCGGAAACCGCGCAGGTGATCATCGCGATGTGTGGGGATGGTGGTTACGGC 1646

Qy 441 MetLeuLeuGlyGluLeuLeuThrValLysValLeuGluHisGlnLeuProleuLysValAlaVal 460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1647 ATGCTGCTCGGTGAGCTTCTGACAGTCAAGGTCCTCGAAATCAGCCGCTTAAGTGTTGCGGTG 1706

Qy 461 PheAsnAsnSerSerLeuGlyMetValLysLeuLeuGluMetLeuValGluGlyGlnGlnGlu 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1707 TTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGACATGCTTGTGGAGGGACAGCCAGAA 1766

Qy 481 PheGlyThrAspHisGluGlyValAsnPheAlaGlnIleIleAlaAlaAlaGlyTyrIleLeuLys 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1767 TTTGGTACTGACCATGAGGAAGTGAATTTCGCACAGAATTGCGCGCCGGTTATCAAA 1826

Qy 501 SerValArgIleThrAspProLysGlyValAsnGluLeuAlaAlaLeuAlaTyr 520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1827 TCGGTACGGATCACCGATCCGAAGGGTGTCAACGAGCTAGCTGAGGCATTGGCCAT 1886

Qy 521 ProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIleProProThr 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1887 CCTGGACCTGTACTGATCGATATCGTAACGGATCCTAATGCGCTGTCGATTCCACCAACC 1946

Qy 541 IleThrTrpGluGlnValMetGlyPheSerIleLysValAlaAlaThrArgThrValPheGlyGly 560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1947 ATCACGTGGGAACAGGTCATGGGATTCAGCATCAAGGTGGCGGCCACCGTCTTTGGTGGA 2006

Qy 561 GlyValGlyAlaMetIleAspPleuAlaArgSerAsnIleArgAsnIleProThrPro 579
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2007 GGAGTAGGAGCGGATGATCGATCTGCGCCGGTTCGATAACATAAGGAATATTCCTACTCCA 2063

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Qy  321  HisValLysGluLysThrAspArgSerPheLeuLeuAspArgMetLeuLysLeuAlaHisGluArg  340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1287  CATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGCTCGCACACGAGGGT 1346

Qy  341  LysLeuSerSerValValGluThrTyrThrHisAsnValGluLysHisValProIleHis     360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1347  AAGTTGAGCTCGGTCGTGGTAGAGACGTACACACATAACGTCGAAGAAGCATGTGCCTATTCAC 1406

Qy  361  ProGluTyrValAlaSerIleLeuAsnGluLeuAlaAspGlyAspAlaValPheThrVal      380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1407  CCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCCGGATAAGGATGCGGTGTTTACTGTG 1466

Qy  381  AspThrGlyMetCysAsnAlaValTrpHisAlaAlaArgTyrTyrIleGluLeuAsnProGlyLeuTyrThrArg 400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1467  GATACCGGCATGTGCAAATGTCTGGCCAATCCGAAGGTACATCCGAGAAGGAGCCGC 1526

Qy  401  AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly     420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1527  GACTTTGTGGGGTTCATTCCCCACGGCACCATGGCTAATCGTCTTCCTCAGCGGATTGGT 1586

Qy  421  AlaGlnSerValAlaAspArgAsnArgGlnValIleIleAlaMetCysGlyValGlyLeuGly  440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1587  GCGCAAAGTGTTGATCGAAACCGCCAGGTCGATCGGGATGTGGCTTGGC 1646

Qy  441  MetLeuLeuGlyLeuGluLeuLeuThrValLysLeuHisGlnLeuProLeuLeuValAlaVal  460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1647  ATGCTGCTGGGGTGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGCTTGTGGTG 1706

Qy  461  PheAsnAsnSerLeuGlyTyrMetValLeuGluMetLeuValGlyGluGlyGlnInProGlu  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1707  TTTAACAACAGTTCTTTTGGGCATGTGAAGTTGGAGATGCTCGTGGGAGAGGGTCAGCCAGAA 1766

Qy  481  PheGlyThrAspHisGluGluValAsnPheAlaLeuIleLeuAlaLeuAlaGlyTyrIleLys  500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1767  TTTGGTACTGACCATGAGGAAGTGAATTTCGCAGAGATTCGGGGTATCAAA 1826

Qy  501  SerValArgIleLeuThrAspProLysValLysArgGluGlnLeuAlaGluLeuAlaAlaTyr  520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1827  TCGGTACGACATCACCGATCCGAAAGAAAGTTCGGCGAGCAGCTGGCTGAGGGCATGGCATAT 1886

Qy  521  ProGlyProValLeuIleAspIleValThrAspProAsnAlaLeuSerIleProProThr    540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1887  CCTGGACCCGTTACTGATCGATATCGTCACGGATCCTAATGCGCTCTCGATCCCACCAACC 1946

Qy  541  IleThrThrProGlnValMetGlyPheSerLysAlaAlaThrArgThrValPheGluGlyGly  560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1947  ATCACGACGCCGGAACAGGTCATGGGATTCAGCAAGGCGGCCACCCGAACCGTCTTTGGTGGA 2006

Qy  561  GlyValGlyValAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro    579
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Db 2007  GGAGTAGGAGGACGGATAACTGGCCGTTCGACATAAGGAAATATTCCTACTCCA 2063
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RESULT 6
US-10-336-049-4
; Sequence 4, Application US/10336049
; Publication No. US20030175911A1
; GENERAL INFORMATION:

; APPLICANT: Hans, Stephan
; APPLICANT: Bathe, Brigitte
; APPLICANT: Reth, Alexander
; APPLICANT: Thierbach, Georg
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Mockel, Bettina

; TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification o
; TITLE OF INVENTION: the zwf Gene
; FILE REFERENCE: 7601/80158
; CURRENT APPLICATION NUMBER: US/10/336,049
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB
US-10-336-049-4

Alignment Scores:
Pred. No.:
Score: 2.28e-272   Length: 2160
Percent Similarity: 2985.00   Matches: 579
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                          15   Gaps: 0

US-09-965-825-2 (1-579) x US-10-336-049-4 (1-2160)

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Qy    1  MetAlaHisSerThrAlaGluGlnLeuIleAspLeuAlaGluThrLeuGlnGlyValLysArg  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  327  ATGGCACACAGCTACGGCAGACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 386

Qy   21  IleTyrGlyLeuValGlyAspSerLeuAsnProIleValArgAlaValArgGlnSerAsp   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  387  ATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTTCGGGCTGTCCGCCAATCAGAT 446

Qy   41  IleGluTrpValHisValArgAsnGluGluAlaAlaAlaPheAlaAlaGlyAlaGluSer   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  447  ATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCGTTTGCAGCGGGTGCAGAATCG 506

Qy   61  LeuLeuThrGlyLeuLeuAlaValCysSerAlaSerCysGlyProGlyAsnThrHisLeu   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  507  TTGATCACTGGGGAGCTGGCCGAGTATGTCGCTTCTTGTGGTCCTGGAAACACACCTG 566

Qy   81  IleGlnGlyLeuTyrAspSerHisArgAsnGlyAlaLysValLeuAlaIleAlaSerHis  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  567  ATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCAT 626

Qy  101  IleProSerAlaGlnIleGlySerThrPheGlnGluThrHisProGluIleLeuPhe      120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  627  AATTCCGAGTGCCAGATAGGTTCGACCTTCCAGGAAACCCATCCGGAGATTTTGTTT 686

Qy  121  LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGlyGlyLysArgIleLeu     140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  687  AAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGCGTGGGGCGAAGGCATTTG 746

Qy  141  HisHisAlaIleGluSerThrMetAlaGlyLysLysGlyValValLysSerValValIlePro  160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  747  CATCACGCGATTCAGTCCACCATGGCGGGGGTAAAGGTGTGTCGGTGGTTAGTGATCCTGGT 806

Qy  161  AspIleAlaLysGluLysGlyAlaGlyAlaGlyAspAlaGlyThrTyrSerAsnSerThrIleSerSerGly  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  807  GATATCGCTAAGGAGAAAGGCGCAGGTGACGGGTACTTAATCCAATTCCACTATTCTTCTGGG 866

Qy  181  ThrProValPheProAspProThrGluAlaLeuAlaAlaLeuValGluAlaIleAlaAsn    200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  867  ACTCCCGTTTTCCCGGACCCCACTGAGGCGCTGGCAGCGCTGGTTGAAGCAATTGCCAAC 926

Qy  201  AlaLysSerValThrLeuPheCysGlyAlaGlyValValAsnAlaArgAlaGlnValLeu    220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  927  GCTAAGTCCGTCACTTTGTTCTGCGGGGCGTGAAGAATGCTCCGCGCGCAGGTGTTG 986

Qy  221  GluLeuAlaGluLysIleLysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIle    240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  987  GAGTTGGCGGAGAAGATTAAATCACCGATCGGGCACGCGCTGGGTGGTAAGCAGTACATC 1046

Qy  241  GlnHisGluAspProGluValGlyMetSerGlyLeuLeuGlyTyrGlyLeuAlaCysVal    260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1047 CAGCATGAGGAATCCGTTGAGGTCGGGCATGCCGGTCTCCTGGGTTACGGGCTGGCGTG 1106

Qy  261  AspAlaLeuSerAsnGluAlaAspLeuLeuLeuLeuLeuGlyThrAspPheProTyrSerAsp  280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1107 GATGCGTTCCAATGAGGGCGGGGATCTGCTCATTCTCATTCTTGGTACCGGATTTCCCTTATTCTGAT 1166
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB
DB: US-10-091-342-4

US-09-965-825-2 (1-579) x US-10-091-342-4 (1-2160)

Alignment Scores:
Pred. No.:
Score: 2985.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 15

Length: 2160
Matches: 579
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Alignment Scores:
Pred. No.:
Score: 2.28e-272
                          2985.00
Percent Similarity: 100.00%   Length: 2160
Best Local Similarity: 100.00%   Matches: 579
Query Match: 16   Conservative: 0
                                           Mismatches: 0
                                           Indels: 0
                                           Gaps: 0

US-09-965-825-2 (1-579) x US-10-686-736-4 (1-2160)

Qy   1 MetAlaHisSerTyrAlaGluValGlnLeuIleAspThrLeuGlnLeuLysArg   20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 327 ATGGCACACAGCTACGCCGAGGTACAGCTGATCGATACCCTGCAGCTGAAGCGA 386

Qy   21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgAsp   40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 387 ATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGGGAT 446

Qy   41 IleGluTrpValHisValArgAsnGluGlnLeuAlaAlaPheAlaAlaGlyGluSer   60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 387 AATTGAGTGGGTGCACGTTCGAAATGAGGAAGGCGGCCGTTTGCAGCCGGTCGGAATCG 506

Qy   61 LeuIleThrGlyGlnLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeu   80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 507 TTGATCACTGGGGAGCTGGCAGTATGTGCCTGCTTCTGTGGTCCTGGAAAACACACTG 566

Qy   81 IleGlnGlyLeuTyrAspSerHisArgAsnGlyAlaLysLeuAlaIleAlaSerHis 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 567 ATTCAGGGTCTTTATGATTCCCATCGAAATGGTGCCAAGTTGGCCATCGCTAGCCAT 626

Qy 101 IleProSerAlaGlnIleLeuGlySerThrPhePheGlnGluThrHisProIleLeuPhe 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 627 ATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAAACGCCATCCGAGATTTGTTT 686

Qy 121 LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGluGlnGlyArgIleLeu 140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 687 AAGGAATGCTCTGGTTACTGCGAGATGGTAAATGGTGGTGAGCAGGGTGAACGCATTTTG 746

Qy 141 HisHisAlaIleGlnSerThrMetAlaGlyValGlySerValValAlaIleProGly 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 747 CATCACGCAGATTCAGTCCACCATGGCCGGCGTTGGCTCCGTCGTGGCGATTCCTGGT 806

Qy 161 AspIleAlaLysGluAspAlaGlyLysAspGlyTyrThrTyrSerAsnSerThrGly 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 807 GATATCGCTAAGGAAGACGCAGGGTACACGTACTCAAACTCCACTAT 866

Qy 181 ThrProValValPheProAspProThrGluAlaAlaLeuAlaLeuLeuValGluAsnAsn 200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 867 ACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCACGCGCTGGTGGAGAGCGGAATAACAC 926

Qy 201 AlaLeuSerValThrLeuProPheCysGlyAlaGlyValGlyAsnAlaArgAlaGlnValLeu 220
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 201 ...

Qy 261 AspAlaSerAsnGluAlaAspLeuLeuIleLeuLeuGlyThrArgAspProTyrSerAsp 280
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1107 GATGCGTCCAAATGAGGCGGATCTGCTGATCCTTCTAGGCACAAGAGATCCTTATTCTGAT 1166

Qy 281 PheLeuProLysAspAlaValAlaLaGlnInValAlaAspIleAsnGlyAlaHisIleGlyTyrArgArg 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1167 TTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGT 1226

Qy 301 ThrThrValLysTyrProValThrGlyAspValAlaLaAlaThrIleGluAsnIleLeuPro 320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1227 ACCACGGTGAAGTATCCCGTGACCGGTGATGTTGCTGCAACAATCGAAAATATTTTGCCT 1286

Qy 321 HisValLysGlyLysThrArgAspArgSerPheLeuValAspArgMetLeuLysAlaHisGluArg 340
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1287 CATGTGAAGGGAAAAACACGAGACCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGCGT 1346

Qy 341 LysLeuSerSerSerValValGluThrThrThrGlyValGluHisHisValProIleHis 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1347 AAGTTGAGCTCGGTTGGTAGAGACCTTACACCATAACGTCACGCCTTATTCAC 1406

Qy 361 ProGluTyrValAlaAlaSerIleLeuAsnGluLeuAlaAspGlyAspAlaValPheThrVal 380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1407 CCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGATAAGGATGCCGTGTTTACTGTG 1466

Qy 381 AspSerThrGlyMetCysSerAsnValTrpHisAlaAspArgTyrIleGluAsnProGluGlyTyrThrArg 400
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1467 GATTCCACGGGCATGTGCAGCAATGTGTGGCACGCTGACAGAATCCGAGAACCGGC 1526

Qy 401 AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1527 GACTTTGTGGGTTCATTCCGCCACGGCACCATGGCTAATGCGTTGCCTCATGCGATTGGT 1586

Qy 421 AlaGlnSerValAspArgAsnArgGlnValIleIleAlaLaMetCysGlyAspGlyGlyLeuGly 440
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1587 GCGCAAAGTGTTGATCGAAACCGCCAGGTGATCATCGCGATGTGTGGCGATGGTGGTTTGGGC 1646

Qy 441 MetLeuLeuGlyGluLeuLeuThrValLysLeuHisGlnLeuProLeuGlyAlaValValVal 460
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1647 ATGCTGCTTGGTGGGGAGCTTCTGACCGTTAAGCTGCACAACTTCCCTCTAGGCGCTGTGGTGGTG 1706

Qy 461 PheAsnAsnAsnSerLeuGlyMetValArgLeuGluGlnMetLeuValGluGlyGlnProGluGlu 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1707 TTTAACAACAGTTCTTTGGGCATGGTGAGGTTGGAGCAGATGTTGGTCGAGGGACAGCCAGAA 1766

Qy 481 PheGlyThrAspHisSerGluGlyValAsnPheAlaGlyIleAlaLaAlaLaAlaGlyTyrLysLys 500
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1767 TTTGGTACTGACCATGAGGAAGTGAATTTCGCAGGAATTGCGGCCGCTGCGGGGTATCAAA 1826

Qy 501 SerValArgIleThrAspProLysLysGluGlnLeuArgGlnGluLeuAlaGluAlaLaThrTyr 520
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1827 TCGGTACGCATCACCGATCCGAAGAAAGTTCGCCAGGAGCACCTAGCTGGACGTTGAGGCCATCTAT 1886

Qy 521 ProGlyProValLeuIleLeuAspIleValThrAspProAsnAlaLeuSerIleProProThr 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1887 CCTGGACCTGTACTGATCACGGATATCGTCACGGACCCTAATGCGCTGTCGATCCCACCAACC 1946

Qy 541 IleThrTrpProGluGlnInValMetGlyPheSerLysAlaLaThrArgThrValPheGlyGly 560
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1947 ATCACGTGGCCAGAACAGGTCATGGGATTCAGCAAGGCGGCCACCCGGACCGTCTTTGGTGGA 2006

Qy 561 GlyValGlyAlaMetIleAspProLeuValLeuArgSerAsnIleArgAsnIleProThrPro 579
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2007 GGAGTAGGAGCGATGATCGATCCGCTTGTCCTTCGAAGCAATATTCGTAACATAAGGAATATTCCTACTCCA 2063

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RESULT 9
US-09-965-825-4
; Sequence 4, Application US/09965825
; Patent No. US20020150999A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Hermann
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID US
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; FILE REFERENCE: 213540SOX
; CURRENT APPLICATION NUMBER: US/09/965,825
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 3248
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (802)..(2538)
; OTHER INFORMATION:
US-09-965-825-4

Alignment Scores:
Pred. No.:
Score:                  3.92e-272       Length:         3248
Percent Similarity:     2985.00         Matches:        579
Best Local Similarity:  100.00%         Conservative:   0
Query Match:            100.00%         Mismatches:     0
                                        Indels:         0
                                        Gaps:           0

US-09-965-825-2 (1-579) x US-09-965-825-4 (1-3248)

Qy     1 MetAlaHisSerTyrAlaGlnGluGlnLeuIleAspThrLeuGluLeuAlaGlnGlyValLysArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   802 ATGGCACACAGCTACGCACAGGAACAATTAATTGACACTTTGGAAGCTCGAAGCGA 861

Qy    21 IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAsp 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   862 ATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCCAATCAGAT 921

Qy    41 MetLeuLeuGlyTyrGluLeuThrValLysLeuHisGlyLeuProLeuLysSerAlaValVal 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   922 AATGCTGCTGGGTGAGCTTCTGACCGTAAGCTGCACCAACTTCCGCCAACTGAGGGAATCG 981

Qy    61 PheAsnAsnSerSerLeuGlyMetLeuValGlyLeuMetLeuValGlyLeuGlnProGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   982 TTGAACAACAGTTCTTTGGGCATGTTGGTCGGTCTCATGCTTGTCGGTCTTCAGCCAGAA 1041

Qy    81 IleGlnGlyLeuLeuTyrAspSerSerHisArgAsnGlyAlaLysValLeuAlaIleAlaSerHis 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1042 ATTCAGGGGTCTTTATGATTCGGCATCGGAAAATGGTGCGAAGGTGTTGGCCATCGCTAGCCAT 1101

Qy   101 IleGluGlyLeuThrGlyGluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1102 ATTGAGGGGCTGACCGGTGAAGCTGTCTGTGCTTGTGCCGGGCCTGGGAATACGCATCTG 1161

Qy   121 LysGluCysPheSerGlyTyrCysGluMetValAsnGlyLysGlyGluAlaTrpValLeuGlnLeu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1162 AAGGAATGTTTCTCTGGTTACTGCGAGATGGTGAACGGTAAAGGGGAGGCATTTG 1221

Qy   141 HisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValAlaValIleProGly 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1222 CATCACGCGGATTCAGTCCACCATGGCCGGGTAAAGGTGTTGTCGGTAGTGGATTCCTGGT 1281

Qy   161 AspIleAlaLysGluAspAlaGlyAlaGlyTyrThrTyrSerAsnSerThrIleSerSerGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1282 ...
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Qy   181 ...
Db  1287 CATGTGAGGAAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTTCAAGCCACACGAGCCT 1346

Qy   381 AspThrGlyMetCysAsnValThrTrpHisSerAlaArgTyrArgIleGluAsnProGluGlyGlyThrArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1347 GATACCGGCATGTGCAATGTGACCTGGCATTCAGCAAGGTACAGGATAGAGAATCCGGAGGGAACGCGC 1406

Qy   361 ProGluTyrValAlaSerPheAlaArgHisGlyThrMetAlaAsnAlaLeuProHisSerAlaIleGlyGly 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1407 CCTGAATACGTTGCCTCTATTTGAACGAGCTGGCGGATAAGGATATCGGTGTTTACCTGTG 1466

Qy   401 AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisSerAlaIleGlyGly 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1467 AAGTTGAGCTCGGTGGTAGAGACCTACACACATAACGTCGAGAAGCAATGTGCCTATTCAC 1526

Qy   421 AlaGlnSerValAspArgAsnArgGlnValIleIleAlaAlaMetCysGlyGlyAspGlyGlyLeuGly 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1527 GCCCAAAGTGTTGATCGGAAAACGCCAGGTCGATGCTGTGGGCGGATGGTTTGGGC 1586

Qy   441 MetLeuGlyGlyLeuLeuThrValLysLeuHisGlyLeuProLeuLysSerAlaValVal 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1587 ATGCTCGGTGGGTGAGCTTCTGACCGTAAGCTGCACCAACTTCCGCCAACTGAGGGAAGTG 1646

Qy   461 PheAsnAsnSerSerLeuGlyMetLeuValGlyLeuMetLeuValGlyLeuGlnProGlu 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1647 TTTAACAACAGTTCTTTGGGCATGTTGGTCGGTCTCATGCTTGTCGGTCTTCAGCCAGAA 1706

Qy   481 PheGlyThrAspHisSerGluGlnValAlaAsnPheAlaGluIleIleAlaAlaAlaGlyIleIleLys 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1707 TTTAACAACAGTTCTTTGGGCATGTTGGTCGGTCTCATGCTTGTCGGTCTTCAGCCAGAA 1766

Qy   501 SerValArgIleThrArgAspProLysValArgGlnLeuAlaGlnValLeuAlaLeuAlaTyr 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1767 TCCGTACGCATCACGCGCGATCCGAAGGTACGGCAGCTGGCACAGGTGCTGGCGCTGGCGTAT 1826

Qy   521 ProGlyProValLeuIleAspIleLeuValLysThrAspProAsnAlaLeuSerIleProProThr 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1827 CCTGGACCTGTACTGATCGATATCGTCAAGACGGATCCCAACGCATTGTCTATCCCACCAACC 1886

Qy   541 IleThrThrTrpGluGlnValMetGlyPheSerArgLysAlaLeuThrArgThrValPheGlyGly 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1887 ATCACGACTTGGGAACAGGTCATGGGATTCAGCAGGAAGGCGCTGACAAGGACGGTTTTCGG 1946

Qy   561 GlyValGlyAlaMetIleGluAspLeuAlaArgSerAsnIleGluArgAsnIleProThrPro 579
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1947 ATACAGTGGGAACAGGTCATGGGATTCAGCAGGAAGGCGCTGACAAGGACGGTTTTGGGA 2006

Qy
Db  2007 GGAGTAGGAGCGATGATCGAGGCTCGGCCGTTCGAACATAAAGGAATATTCCTACTCCA 2063
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RESULT 10
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-1

Alignment Scores:
Pred. No.:
Score: 3.96e-268
Percent Similarity: 2985.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9

Length: 3309400
Matches: 579
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-965-825-2 (1-579) x US-09-738-626-1 (1-3309400)

[rotated DNA/protein sequence alignment data — Qy (query) and Db (database) paired lines with residue translations and base numbering]

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Qy    101 IleProSerAlaGlnIleIleGlySerThrPhePheGlnGluThrHisProGluIleIlePhe 120
          ATTCCGAGTGCCCAGATTATTGGTTCCACATTCTTCCAGGAAACCCATCCGGAGATTATTTTT
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db 2778204 ATTCCGAGTGCCCAGATTATTGGTTCCACATTCTTCCAGGAAACCCATCCGGAGATTATTTTT 2778145

Qy    121 LysGluCysSerGlyTyrCysGluMetValAsnGlyValGlyLnGlyGluArgIleLeu 140
          AAGGAAAATGCTCTGGTTACTGCCGAGATGGTGAATGGTGTGGGTGAAGGACGCATTTTG
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2778144 AAGGAAAATGCTCTGGTTACTGCCGAGATGGTGAATGGTGTGGGTGAAGGACGCATTTTG 2778085

Qy    141 HisHisAlaIleGlnSerThrMetAlaGlyLysGlyValSerValValIleProGly 160
          CATCACGCGATTCAGTCCACCATGGCCGGGTAAAGGTGTGTCGGTGGTGATTCCTGGT
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db 2778084 CATCACGCGATTCAGTCCACCATGGCCGGGTAAAGGTGTGTCGGTGGTGATTCCTGGT 2778025

Qy    161 AspIleAlaLysGluAspAlaGlyAspGlyTyrTyrSerAsnSerThrGly 180
          GATATCGCTAAGGAAGACGCAGGGGACGGGTACTATTCCAATTCCACTGGT
          ||||||||||||||||||||||||||||||||||||||||||
Db 2778024 GATATCGCTAAGGAAGACGCAGGGGACGGGTACTATTCCAATTCCACTGGT 2777965

Qy    181 ThrProValPheProAspProThrGluValAlaAlaLeuValGluAlaIleAsnAsn 200
          ACTCCTGTGTTCCCGGATCCTACTGAGGTGGCTGCGCTGGTGGAGGCGATTAACAAC
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777964 ACTCCTGTGTTCCCGGATCCTACTGAGGTGGCTGCGCTGGTGGAGGCGATTAACAAC 2777905

Qy    201 AlaLysSerValThrLeuPheCysGlyTyrAlaGlyValValLysAsnLeuArgGlnAlaGlnValLeu 220
          GCTAAGTCTGTCACTTTGTTCTGCGGCTATGCGGGCGTGGTGAAGAATCTGCGGCAGGTGTTG
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777904 GCTAAGTCTGTCACTTTGTTCTGCGGCTATGCGGGCGTGGTGAAGAATCTGCGGCAGGTGTTG 2777845

Qy    221 GluLeuAlaGlyLysIleLysSerProIleGlyHisAlaLeuGlyLysLysGlnThrYrIle 240
          GAGTTGGCCGGGAAGAGNTTAAATCACCCGGATGCGGCTGGGGTGGGTAAGCAGTACATC
          ||||||||||||||||||||||||||||||||||||||| |||||||
Db 2777844 GAGTTGGCCGGGAAGAGNTTAAATCACCCGGATGCGGCTGGGGTGGGTAAGCAGTACATC 2777785

Qy    241 GlnHisGluAsnProPheGluValGlyMetSerGlyTyrLeuLeuLeuGlyTyrGlyTyrAlaCysVal 260
          CAGCACGAGAATCCGTTTGAGGTCGGCATGTCTGGCTATCTGCTTGGTTACGGCTGCGTG
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777784 CAGCACGAGAATCCGTTTGAGGTCGGCATGTCTGGCTATCTGCTTGGTTACGGCTGCGTG 2777725

Qy    261 AspAlaSerAsnGlyValLysAspLeuLeuIleLeuLeuGlyTyrThrArgPheProTyrSerAsp 280
          GATGCGTCCAATGAGGGCGTTAAGGACCTGCTGATTCTTATTGGGTACGGACGGTTCCCTTATTCTGAT
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777724 GATGCGTCCAATGAGGGCGTTAAGGACCTGCTGATTCTTATTGGGTACGGACGGTTCCCTTATTCTGAT 2777665

Qy    281 PheLeuProLysAspAsnValAlaLeuGlnValValAspAspIleAsnGlyIleAlaHisIleGlyArgArg 300
          TTCCTCCCTAAAGACAACGTTGCCCAGGTGGATATCAACGGTGCCCACATTGGTCGACGT
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 2777664 TTCCTCCCTAAAGACAACGTTGCCCAGGTGGATATCAACGGTGCCCACATTGGTCGACGT 2777605

Qy    301 ThrThrValTyrProValThrGlyAspValAlaAlaLeuThrIleGluAsnIleLeuPro 320
          ACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCACAAATCGAAAATATTTTGCCT
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777604 ACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCACAAATCGAAAATATTTTGCCT 2777545

Qy    321 HisValLysGlyLysThrAspSerPheLeuAspArgMetLeuGlyAlaHisGluArg 340
          CATGTGAAGGGAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCGGAGCACACGAGCGT
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777544 CATGTGAAGGGAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCGGAGCACACGAGCGT 2777485

Qy    341 LysLeuSerSerValValGluThrTyrThrHisAsnValGluLeuValLysProHisHis 360
          AAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTTGAACTGGTCAAGCCATCTCAT
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777484 AAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTTGAACTGGTCAAGCCATCTCAT 2777425

Qy    361 ProGlyProValLeuValLeuAsnGluLeuAlaSerProAlaValPheThrVal 380
          CCTGGACCGGTTCTTGTCCTTAATTTGAACAGACCGGCGGTTTTACTGTG
          |||||||||||||||||||||||||||||||||||||||||||||
Db 2777424 CCTGGACCGGTTCTTGTCCTTAATTTGAACAGACCGGCGGTTTTACTGTG 2777365

Qy    381 AspThrGlyMetCysGlyAsnValTrpHisAlaArgTyrIleGluAsnProGluGlyThrArg 400
          GATACCGGCATGTGCGGTAGTGTGCCCGGATGGCAGGTGTACATCGAGAATCCGGAAGGAACGCGC
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777364 GATACCGGCATGTGCGGTAGTGTGCCCGGATGGCAGGTGTACATCGAGAATCCGGAAGGAACGCGC 2777305

Qy    401 AspPheGlySerPheHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly 420
          GACTTTGGGTCATTCCACGGCACGATGGCTAATGCCCTCCATGCGATTGGT
          |||||||||||||||||||||||||||||||||||||||||||||||
Db 2777304 GACTTTGGGTCATTCCACGGCACGATGGCTAATGCCCTCCATGCGATTGGT 2777245

Qy    421 AlaGlnSerValAspArgAsnArgGlnValIleIleAlaMetCysGlyAspGlyGlyLeuGly 440
          GCGCAAAGTGTTGATCGGAAACCGCAGGTGATCGCGATCTGTGTGGGCGATGGTGGTTTGGGC
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777244 GCGCAAAGTGTTGATCGGAAACCGCAGGTGATCGCGATCTGTGTGGGCGATGGTGGTTTGGGC 2777185

Qy    441 MetLeuLeuGlyGluLeuLeuThrValLeuGluHissGlnLeuProLeuLysLysAlaValVal 460
          ATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGAAGAAGGCTGTGGTG
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777184 ATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAACTTCCGCTGAAGAAGGCTGTGGTG 2777125

Qy    461 PheAsnAsnSerLeuGlyMetValLysLeuGluMetLeuValGlyGlyGlnProGluGlu 480
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RESULT 11
US-10-282-122A-17635

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Qy    481 PheGlyTyrThrAspHisGluHisValAsnPheLeuGlnLeuAlaGluAlaAlaGlyIleLys 500
          TTTGGTTACACTGACCATGAGCATGTGAATTTCCTGCAGCTTGCCGAGGCTGCCGGGATCAAA
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777064 TTTGGTTACACTGACCATGAGCATGTGAATTTCCTGCAGCTTGCCGAGGCTGCCGGGATCAAA 2777005

Qy    501 SerValArgIleThrAspProGlyLysValArgGlyLnLeuAlaGlyAlaLeuAlaTyr 520
          TCGGTACGCATCACCGATCCCAAGAAAGTTCGCGGACAGCTGGCGGGTGCCCTGGCATAT
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2777004 TCGGTACGCATCACCGATCCCAAGAAAGTTCGCGGACAGCTGGCGGGTGCCCTGGCATAT 2776945

Qy    521 ProGlyProValLeuLeuAspIleGlnValThrAspAspProAsnAlaLeuSerIleProProThr 540
          CCTGGACCTGTACTGCTGGATATCCAGGTCACCGATGATCCTAATGCGCTGTCGATTCCACCAACC
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2776944 CCTGGACCTGTACTGCTGGATATCCAGGTCACCGATGATCCTAATGCGCTGTCGATTCCACCAACC 2776885

Qy    541 IleThrTrpGluGluValMetGlyPheSerGlyLysAlaAlaThrArgThrValPheGlyGly 560
          ATCACCTGGGAAGAAGTGATGGGATTCAGCGGCAAGGCCGCCACCCGAACCGTCTTTGGTGGA
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2776884 ATCACCTGGGAAGAAGTGATGGGATTCAGCGGCAAGGCCGCCACCCGAACCGTCTTTGGTGGA 2776825

Qy    561 GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleAlaArgAsnIleProThrPro 579
          GGAGTAGGAGCGATGATCGACCTGGCCCGTTCGAACATATAAGGAAAATATTCCTACTCCA
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2776824 GGAGTAGGAGCGATGATCGACCTGGCCCGTTCGCCCGTTCGAACATATAAGGAAAATATTCCTACTCCA 2776768
```

Alignment Scores:

Pred. No.:	1.03e-207
Score:	2300.50
Percent Similarity:	86.18%
Best Local Similarity:	74.27%
Query Match:	77.07%
DB:	16

Length:	1734	
Matches:	430	
Conservative:	69	
Mismatches:	79	
Indels:	1	
Gaps:	1	

US-09-965-825-2 (1-579) x US-10-282-122A-17635 (1-1734)

```
Qy    1  MetAlaHisSerTyrAlaGlyHisLeuIleAspThrLeuGlnGlyValValLysArg  20
         |||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db    1  ATGGCAAAAAATTTTGGGGAACATCGTAGAAGCTTGGAAAAACAGAGTAAAGCGC  60

Qy   21  IleTyrGlyLeuValGlyAspSerLeuAsnProIleValAspAlaValArgGlnSerAsp  40
         |||||:||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   61  ATCTACGGTTTGGTCGGAGATAGCCTCAACCCGATCGTGGATGCAGTACGCCACCTCCAAC  120

Qy   41  IleGluTrpValHisValAlaArgAsnGluGluAlaAlaAlaGlyValAlaGluSer  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ATCGAATGGGTTCACGTTGCGCGCAATGAGGAAGCAGCCGCAGGAAGCAGAAAGC  180

Qy   61  LeuIleLeuThrArgGlyGluLeuAlaValCysAlaAlaSerCysGlyProGlyAsnThrHisLeu  80
         |||:||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db  181  CTGCTCACCCGCGAACTAGCTGTCTGTGCAGCCTCTTGCGGCCCTGGAAATACCCACCTC  240

Qy   81  IleGlnGlyTyrAspSerHisSerArgAsnGlyValAlaLysValLeuValIleAlaSerHis  100
         ::||||||||||||||||||||||||||||||||||||||||||||||:::
Db  241  GTCCAAGGGTTCTTACGACGGCCACAGTAACCGGCCAAAGTACTCGCCACCTCCCACCACC  300

Qy  101  IleProSerAlaGlnIleLeuGlySerThrPhePheGlnThrHisProGlnIleLeuPhe  120
         ::::|||||||||||||||||||||||||||||||||||||||||||||||
Db  301  ATTCCCTCACGCGCAAATCGGCTTCACATTCTTCCAAGAACCACCCCAGAGCCCCTTCTTT  360

Qy  121  LysGluCysSerGlyTyrCysGluMetValAsnGlyGlyGlnGlyGluArgIleLeuLeu  140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GCTGAGTGCTCCGGCTACTGCGAAATGGTAACTCGCCACTCCAGGGGTGAGCGTCATCTTG  420

Qy  141  HisHisAlaIleGlnSerThrMetAlaGlyLeuTyrTyrSerAsnSerThrIleSerProGly  160
         |||||||||||||||||||||||||||||||||:::|||||||||
Db  421  CACCACGCCATCCAGTCGACCATGGCTGGCCTGTATTACTCCAACAGCACCATCTCCAGGC  480

Qy  161  AspIleAlaLysGlyLeuAspProAlaAlaGlyAspGlyTyrTyrSerAsnSerThrIleLeuSerSerGly  180
         |||||||||||||||||||||||||||||||||:::|||||||||
Db  481  GATGTGACCATGGCAAGACGTGGAGGACGACACCTTCACCGGTTCGCGGGATTCCCAGGC  540

Qy  181  ThrProValValPhePheLeuProAspProThrGluAlaAlaAlaLeuValGluAlaIleLeuAsnAsn  200
         ||||||||||||||||||||||||||||||||||::|||||||||||||
Db  541  CGTCCCATCAGTGTACCCAGCCAGTCTGAGCCGCGACCTGGCTCAAAGCCATCAACGAG  600

Qy  201  AlaLysSerValThrLeuPheCysGlyValValValLysAsnAlaAlaArgAlaAlaGlnValLeu  220
         :::||||||||||||||||||||||||||||||||::::
Db  601  GCCAAAAACCGTCACTTGTTTGTTGGCGGTGGCGCCGAAAGAAGTTCCTC  660

Qy  221  GluLeuAlaGlyLysIleLeuLysSerProIleGlyHisAlaLeuGlyLysGlnTyrIle  240
         ||||||||||||||||||||||||||||||||||||||||||||
Db  661  GAACTCGCAGAAAAGATCAAAGGACACCCATGGGCCCACGCTCTGGGCAAAAATGTACATC  720

Qy  241  GlnHisGlyAsnProGluGlyValGlyMetSerGlyLeuLeuGluGlyTyrGlyValAlaCysVal  260
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  CAGTACGGACACCCCTTTGGACGTGGGGCATGTCCGGGCCTACGGAGGCCTGGCCAC  780

Qy  261  AspAlaSerArgAsnGluAlaAspLeuLeuIleLeuGlyThrArgPheProTyrSerAsp  280
         ||||||||||||||||||||||||||||||||||||||||||||||||::
Db  781  GACGGCTTCCAACGACCCGGACCTGCTGATCCTCCCCGGCACGAGACTACGAC  840

Qy  281  PheLeuProLysAspAsnValAlaGlnValAlaLysAspIleAlaSerGlyAsnGlyValAlaHisIleGluGlyTyrArgArg  300
         |||||||||||||:::||||||||||||||||||||||||||||||||
Db  841  TTCTTGCCCAAGGACAACGTTGCACAGATCGACATCGCACGCCCCGGC  900

Qy  301  ThrThrValGlyTyrProValThrGlyAspValAlaAlaAlaThrIleGluUsnIleLeuPro  320
         |:||||||||::::||||||||
Db  901  ACCCGCCATCAGCCACCCCTGTGGTTGGCGACGGTTGCCGCAACAAATTCGGACATCTCCG  960
```

```
Qy  321  HisValLysGluGlyLysThrAspArgSerPheLeuAspArgAspArgMetLeuGlyLysAlaHisGluArg  340
         |||||||:::|||||||||||||||||||||||::||||||||||||||:::
Db  961  CACATCGAGGGAAAAAGACTGACCGTTCCTTCCTCCGACCGGCCGCTGCTGAAAAAGGCATCACGC  1020

Qy  341  LysLeuSerSerValValGlyThrTyrThrHisAsnValGluLysHisValProIleHis  360
         |||||||:::|||||||||||||||||||||||||||||||||||||||
Db 1021  AAGCTTAACGACGTGATCGAGGGCTACACCTCAGGGGTGGAGAAGCACACCCCTATCCAC  1080

Qy  361  ProGluTyrValAlaSerIleLeuAsnGluLeuAlaLeuAlaAspLysAspAlaValPheThrVal  380
         ||||||:::|||||||||||||||||||:::||||||||||||||||
Db 1081  CCAGAATTGTGGCCAACATTATCGACGAAATCGCCCGGCGTATCACGG  1140

Qy  381  AspThrArgGlyMetCysAsnValThrProHisSerAlaArgThrTyrrIleGluAsnProGluGlyThrArg  400
         |||:::||||||||||||||||||||||||||---|||||||||
Db 1141  GATACCCGGCCATGTGCACGTTTGGGGGTGCTCCCTACATC---ACCCCTAATGCACACGT  1197

Qy  401  AspPheValGlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleGly  420
         ::|||||||||||||||||||||||||||||||||||||||||||
Db 1198  GAAAATGATCCGGTCTCGTTCCGCCACGGGCACCATGGCGAATGCGCTGCCACACGCTATCGGC  1257

Qy  421  AlaGlnSerValAspArgAsnAsnArgGlnValIleAlaAlaMetCysGlyAspGlyGlyTyrLeuGly  440
         ||||||:::||||||||||||||||||||||||||||||||::||
Db 1258  GCATCTCGTCGCTAACCCAAGAGTCAGGTTGTCACCTTGTCGGCCATGGGGTATCGGC  1317

Qy  441  MetLeuLeuGlyGluLeuLeuThrValLysLeuHisGlnIleLeuProLeuLysLysValVal  460
         |||||||||||||||||||||||||||||||||||||||||||:::
Db 1318  ATGCTCATGGGCGAGCTGCTCACTGTTAAGCTGCACAACCTTCCTATTAAAGACTGTTGTG  1377

Qy  461  PheAsnAsnSerLeuGlyMetValLysGluMetLeuValGlyGlnGluProGlu  480
         ||||||::||||||||||||||||||||||||||||||||||:::
Db 1378  TTTAACAACTCCTCGGTCAAGGCTGAAGCTGGAAAATCGGTTCAGGGGCCAGAG  1437

Qy  481  PheGlyThrArgPheHisGluGluValPheGluAlaGlyIleLeuAlaLysAlaAlaGlyIleLeuLys  500
         ||||||:::||||||||||||||||||||||||||||||||||||
Db 1438  CACGAAACTGATCATGGACATGGACTTTGACGCCTGCAGTGGGTATCGAG  1497

Qy  501  SerValArgIleThrAspProLeuLysValArgGluGlyAlaGluThrIleGluProPro  520
         |||||||:::||||||||||||||||||||||||||||||
Db 1498  CACATTAAGATTAACGGACCCCGACTAAGGCACGTCACAGCGAGCCATTGATTAT  1557

Qy  521  ProGlyProLeuLeuAspIleValAsnGlyPheSerLysAlaAlaThrArgThrValPheGlyGly  540
         |||:::||||||||||||||||||||||||||||||||||||||||
Db 1558  GACGGGTCCTGTCCTGGATCGGAAGCATCACATCACTGACCCTTGTCGATCCCACCGGAAC  1617

Qy  541  IleThrThrTrpGluGlnIleValMetGlyPheSerLysAlaAlaThrArgThrValPheGlyGly  560
         ||:::||||||||||||||||||||||||||||||||||||||||||
Db 1618  ATCACACGATGGAATATGGCTTGATGGGCTTCTCTGCAGCTACGCGCACTGTTTTCGGTGGC  1677

Qy  561  GlyValGlyAlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro  579
         |||||||:::||||||||||||||||||||||||||||||||||
Db 1678  GGCGTGGGCGCCACATGGTTAGATATGGCGAAGTCCAATCTGCGTAACATTCCAAAGCCA  1734
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; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2067
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-10-156-761-2067

Alignment Scores:
Pred. No.:
Score:                   3.12e-155
                         1746.00
Percent Similarity:      74.13%
Best Local Similarity:   58.68%
Query Match:             58.49%
DB:                      15

US-09-965-825-2 (1-579) x US-10-156-761-2067 (1-1740)

                                    Length:           1740
                                    Matches:          338
                                    Conservative:     89
                                    Mismatches:       145
                                    Indels:           4
                                    Gaps:             4
```

```
Qy      6 AlaGluGlnLeuIleAspThrLeuGlnLeuGluAlaGlnGlyGlyValLysArgIleThrTyrGlyLeuVal 25
            |||||  ||||||||  |  |||||      ||  |||||||||||||||
Db     19 GCCGAGCAGTTGTTGACATCCTCGTCCGGCCGGGTCAATACGCCTGTACGGGGTGGGTG 78

Qy     26 GlyAspSerLeuAsnProIleValAspAlaValArgGln---SerAspIleGluTrpVal 44
            |||||||||||||||    |||||||||||||||||:::     ||||||
Db     79 GGTGACAGTCTCAACCCGGTCGTCGACGCCGTCAGGCAACTCCGACATCGACTGGATC 138

Qy     45 HisValArgAsnGluGluLeuAlaPheAlaAlaGlyAlaGluSerLeuThrArgGly 64
            |||||  |||||||||||||||||||  |:|||
Db    139 CACGTCCGGAACGAGGGGCTCGCCTTCGCCGCGGGCGCGGAGATCACCGGC 198

Qy     65 GluLeuAlaValCysAlaLaAlaSerCysGlyProGlyAsnThrHisLeuIleGlnGlyLeu 84
            :::||||   ||  |||||||||||||||||||||||||||:::
Db    199 AAGCTCGCCGCGTGCGCCGGCCTCCTGGGCCCGGGAAACCTCACCTCATCAACGGCCTG 258

Qy     85 TyrAspSerHisArgAsnGlyValAlaLysValLeuValLeuGlyProSerAla 104
            ||||  ||||||  :::||||  ||||||||||||||||:::
Db    259 TACGACAGCCACCGCTTCCAACGGCGGGTCCTCGCCACATCCCCTCCAGC 318

Qy    105 GlnIleGlySerThrPhePheGlnLeuThrHisProGluLeuPheLysGluCysSer 124
            :||||||||||||||||  ||||||||||||||||||||:::
Db    319 GAGATCGGCTCGACCTTCTTCCAGGAGACCCATCCCGAGCTGTTCAAGGAGTGCAGT 378

Qy    125 GlyTyrCysGluMetValAsnGlyIleGlyGlnGlyIleArgIleLeuHisHisAlaIle 144
            ||||||   ||||  ||||  ||||||||||||||:::
Db    379 CACTACAGCGACGAGATGATCTCCAACCCGGAACCGAGGGTCTGGCAGTCGCCATC 438

Qy    145 GlnSerThrMetAlaGlyLysGlyValSerValValLeuIleProGlyAspIleAlaLys 164
            ||  |||    |||     ||:::||  |||||  ||||||:::
Db    439 CAGCACGACGCGGTCGGGTGGTCAGGGTTCAGGTGGTCACCCTGCGCCTCC 498

Qy    165 GluAspAlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrProVal 184
            |||||     ||:::  ||||||||||||||||:::
Db    499 GAGGCCCGCCCCGACACAAGGCCGTCGAGACCGCCCTCGTCAGCTCC 555

Qy    185 PheProAspProThrGluAlaIleAlaAlaLeuValGluAlaIleAsnAsnAlaLysSerVal 204
            ||    |::  ||:::|||||||||||||::|
Db    556 CGGCCCCGGCCGACACCGAGATCGACGCGTCCGGTTGATCGACGCAAGGTC 615

Qy    205 ThrLeuPheCysGlyValAlaGlyValAlaLysAsnAlaArgAlaGlnValLeuGluGlyLeuAlaGlu 224
            ||:::  ||||||||||||||  :::|||||||||||||
Db    616 ACCCTCTTCTGCGGCGTCGCGGGCGTGGCCAAGAACGCGCGGGCGCAGGTGCTCGAGGGTTCGCGCGAG 675

Qy    225 LysIleLeuSerProIleGlyHisAlaLeuGlyLeuTyrIleGlnThrTyrGlnHisGlnAsn 244
            ||||||||||||||||||:::  ||||||||||:::
Db    676 AAGATCAAGTCCCCGATCGGGCACGCGCTGGGCCTGTACATCCAGACGTACCAGCAC 735

Qy    245 ProPheGluValGlyMetSerGlyLeuLeuGlyTyrGlyValCysValAspAlaSerAsn 264
            ||||||||||||||||||||||||||||:::
Db    736 CCGTTCGAGGTCGGCATGAGCGGCCTCCTCGGCTACGGCGTGTGCGTCGATGCCAGCAAC 795

Qy    265 GluAlaAspLeuLeuIleLeuLeuGlyThrAspPheProTyrSerAspPheLeuProLys 284
```

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Db    796 GAGTGCGGATCCTGCTGGAT...
                |||||||||||||||  |||||||
...
Qy    285 Asp---AsnValAlaGlnValAlaAspIleAsnGlyAlaAlaHisIleIleGlyArgArgThrArgVal 303
            :::||||||||||||||||||||::
Db    856 GAATGGAAGATCGCACAGGTCGCAGACATCAACGGCGCCGCCCACATCATCGGGCGGCGGACGCGCGTG 915

Qy    304 LysTyrProValThrGlyAspValAlaAlaAlaThrThrIleGluAsnIleIleLeuProHisValLys 323
            ||||||||||||||  ||||  ||:::||||||||||||||||||||:::
Db    916 GACCTCGCCCGTCTGGGGGACGTGGCCGACCCTGCGTGTCTGATCCCGCATGTGAAG 975

Qy    324 GluLysThrArgAspArgSerPheLeuAspArgMetLeuLysPheThrValAspThrValGly 343
            :::||||||||||||||||||||||:::
Db    976 CCCAAGCGAGAACCGCGCTTCCTCGACAGATGCTGAAGTTCACCGTCGACACCGTTGGG 1035

Qy    344 SerValValGluThrTyrThrHisAsnValGlyLysHisIleValProIleHisProGluTyr 363
            :::||||||||||||||||||||||||||:::
Db   1036 GGTGTCATCAAGGCCGTACACCGGGAGGACGTGCGGACCCTGCGTGTCTGATCCCGCACGTGAGTAC 1095

Qy    364 ValAlaSerIleLeuAsnGlyLeuAlaAspLysSerAspAlaValPheThrValAspThrArgGly 383
            ||||||||||||||||  :::|||||||||||||
Db   1096 GTGGCCTCCATTCTCGAACGGCCTGGCCGACAAGAGCGACGCGGTGTTCACCGTCGACAC 1155

Qy    384 MetCysAsnValTrpHisAlaAsnArgTyrIleGluAsnProGluGlyThrArgAspPheVal 403
            |||||||||||  |||||||||||||:::
Db   1156 ATGTGCAAATGTTCTGGGACGCGCCGCTACATC---TCGCCAACGAGGCGACGCGTCATC 1212

Qy    404 GlySerPheArgHisGlyThrMetAlaAsnAlaLeuProHisAlaIleIleGlyAlaGlnSer 423
            |||||||||||||||||||||||||::|
Db   1213 GGCTCGTTCCGGCACGGCACGATGGCGAACGCGCTGCCCCATGCGATCATCGGCGCGCAGTCC 1272

Qy    424 ValAspArgAsnArgGlnIleValIleIleAlaLeuMetCysGlyAsnGlyGlyLeuMetLeuLeu 443
            ||||||||||||||||  :::|||||||||||||
Db   1273 ACCGACCGGAACCGGCAGATCGTCGTGATCGCGCTGATGTGCGGGAACGGCGGGCTGATG 1332

Qy    444 GlyGluLeuLeuPheHisValValLeuLeuHisGlyIleAsnLeuProLeuHisLysValValValPheAsnAsn 463
            |||||||||||||||||||||  :::
Db   1333 GGCGAGCTCCTCACCCTCGTCCAGTACGAACCTGCGGTGGAGGTCGTTACTGTTCAACAAC 1392

Qy    464 SerSerLeuGlyMetValLysArgGluGlnGluMetLeuValIleGlnGlyAlaGluGlyThr 483
            ||||||||||||||||:::  |||||||||||||
Db   1393 TCCTCGCTGGGCATGGTCAAGCGCGAGTTGGAGATGCTGGTCATCCAGGGCGCCGAGGGGACG 1452

Qy    484 AspHisAlaGluGluValAsnPheAlaGluIleIleAlaAlaLeuAlaGlyIleLysLysSerValArg 503
            |||||||||||||||||||:::
Db   1453 ACGAACGAGGAGGTGAACTTCGCGGAGATCATCGCCGCGCTGGCCGGGATCAAGAAGTCGGTGCGC 1512

Qy    504 IleThrAspProLysLysValArgGluGlnIleGlnLeuAlaLeuAlaTyrProGlyPro 523
            :::||||||||||||||||||||||
Db   1513 GTCACGGACCCGAAGAAGGTGCGCGAGCAGATCCAGCTCGCGCTGGCTTACCCGGGGCCG 1572

Qy    524 ValLeuIleAspProAlaAsnAlaLeuSerIleLeuProThrIleThrTrp 543
            ||||||||||||||||||  :::
Db   1573 GCCCTCGTCGACCCCGCCAACGCGCTGTCCATCCTGCCGACCATCACCTGG 1632

Qy    544 GluGlnValMetGlyPheSerLysAlaLeuAlaThrArgThrValPheGlyGlyGlyValGlyGly 563
            |||||||||||:::|||||||||||:::
Db   1633 GAGCAGGTGATGGGCTTCTCGAAGGCCCTGGCGACGCGGACGGTGTTCGGCGGCGGCGTCGGCGGC 1692

Qy    564 AlaMetIleAspLeuAlaArgSerAsnIleArgAsnIleProThrPro 579
            ||:::||||||||||||||||||:::
Db   1693 CGGATGGGTGCAGATGGCCCGGCTCCACCGTGGGAACGGTGGCCGCTCCT 1740
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RESULT 13
US-10-156-761-1/c
Sequence 1, Application US/10156761
Publication No. US20030119018A1
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```
; APPLICANT:  SAKAKI, YOSHIYUKI
; APPLICANT:  HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE:  2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
;   LENGTH: 9025608
;   TYPE: DNA
;   ORGANISM: Streptomyces avermitilis
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: (4187715)
;     OTHER INFORMATION: a, t, c, g, other or unknown
; US-10-156-761-1

Alignment Scores:
Pred. No.:
Score:                1746.00
Percent Similarity:   74.13%
Best Local Similarity: 58.68%
Query Match:          58.49%
DB:                   15

US-09-965-825-2 (1-579) x US-10-156-761-1 (1-9025608)
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RESULT 14

US-10-781-014-89

; Sequence 89, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: BGI-126CPCN
; CURRENT APPLICATION NUMBER: US/10/781,014
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 09/602,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/143,208
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/151,572
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931412.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931424.1
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931428.4
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 89
; LENGTH: 944
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION: FRXA00635

US-10-781-014-89

Alignment Scores:
Pred. No.:
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Best Local Similarity:　100.00%
Query Match:　　　　100.00%
DB:　　　　　　　　53.27%

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US-09-965-825-2 (1-579) x US-10-781-014-89 (1-944)

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Qy　293 AsnGlyAlaHisIleGlyArgArgThrThrValTyrProValThrGlyAspValAla 312
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Qy　313 AlaThrIleGluAsnLeuProHisValLysGluLysThrArgSerPheLeuAsp 332
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Qy　333 ArgMetLeuLysAlaHisGluArgLysGluSerSerValValGluThrTyrThrHisAsn 352
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Qy　353 ValGluLysHisValProIleHisProGluTyrValAlaSerIleLeuAsnGluLeuAla 372
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Db　241 GTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCG 300

Qy　373 AspLysAspAlaValPheThrValAspThrGlyMetCysAsnValTrpHisAlaArgTyr 392
　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　301 GATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCACGCGAGGTAC 360

Qy　393 IleGluAsnProGluGlyThrArgAspPheValGlySerPheArgHisGlyThrMetAla 412
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Db　361 ATCGAGAATCCGGAGGGAACGCGCGACTTTGTCGGGTCGTTCAGGCACGGCACGATGGCT 420

Qy　413 AsnAlaLeuProHisAlaIleGlyAlaGlnSerValAspAspAsnArgGlnValIleAla 432
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Db　421 AATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATGACAACCGGCAAGTGATCGCG 480

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Qy　453 GlnLeuProLeuLysGlyAlaValValPheAsnAsnSerSerLeuGlyMetValLeuGlu 472
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Db　661 ATTGCGGCGGCGGCTGGCGGGTATCAAAATCGGTACGCATCACCAGAAGAAAGTTCGCGAG 720

Qy　513 GlnLeuLeuAlaGluAlaLeuAlaTyrProGlyProValLeuIleAspIleValThrArgPro 532
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Db　721 CAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATATCCGATATCGTTACGCGATCCT 780

Qy　533 AsnAlaLeuSerIleProProThrIleThrTrpProGlnLnValMetGlyPheSerLysSerAla 552
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Qy　553 AlaThrArgGlnThrValPheGlyLyGlyValGlyValAlaMetIleAspLeuValAlaArgSerAsn 572
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Db　841 GCCACCCGACAGCGTCTTTGGTGGAGGAGTGAGGAGGCGGATGATCGATCTGGCCGGTTCGAAC 900

Qy　573 IleArgAsnIleProThrPro 579
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Db　901 ATAACGAAAATATTCCTACTCCA 921

RESULT 15

US-09-965-825-3

; Sequence 3, Application US/09965825
; Patent No. US20020150999A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Hermann
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID US
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; FILE REFERENCE: 21354USOX
; CURRENT APPLICATION NUMBER: US/09/965,825
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum

US-09-965-825-3

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Query Match:　　　　　100.00%　　　Mismatches:　0
DB:　　　　　　　　　50.85%　　　　Indels:　　　0
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US-09-965-825-2 (1-579) x US-09-965-825-3 (1-875)

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Qy   147 ThrMetAlaGlyLysGlyValSerValValIleProGlyAspIleAlaLysGluAsp 166
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Qy   167 AlaGlyAspGlyThrTyrSerAsnSerThrIleSerSerGlyThrProValValPhePro 186
Db   121 GCAGGTGACCGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTCGTTGTTCCG 180

Qy   187 AspProThrGluAlaAlaAlaLeuValGlnAlaIleIleAsnAlaAlaLysSerValThrLeu 206
Db   181 GATCCTACTGAGGCTGCAGCGCGTGGGTGGAGCGGATTAACAACGCTAAGTCTGTCACTTTG 240

Qy   207 PheCysGlyAlaGlyValLysAsnAlaAlaArgAlaGlnValLeuGluLeuAlaGluLysIle 226
Db   241 TTCTGCGGTGCGGGGTGAAGAATGCTGCGCGCCAGGTGTTGGAGTTGGCGGAGAAGATT 300

Qy   227 LysSerProIleGlyHisAlaLeuGlyGlyLysGlnTyrIleGlnHisGluAsnProPhe 246
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Qy   247 GluValGlyMetSerGlyLeuLeuGlyTyrGlyAlaCysValAspAlaSerAsnGluAla 266
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Qy   267 AspLeuLeuIleLeuLeuGlyThrAspPhePheLeuProLysAspAsn 286
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Qy   307 ValThrGlyAspValAlaAlaThrIleGluAsnIleLeuProHisValLysGlyLysThr 326
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Qy   327 AspArgSerPheLeuAspArgMetLeuGlyLysGluArgGlyLysLeuSerSerValVal 346
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Qy   347 GluThrTyrThrHisAsnValGlyLysHisValProIleHisProGluTyrValAlaSer 366
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Qy   367 IleLeuAsnGluLeuAlaAspLysAspAlaValPheThrValAspThrGlyMetCysAsn 386
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Qy   387 ValTrpHisAlaArgTyrIleGluAsnProGluGlyThrArgAspPheValGlySerPhe 406
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Qy   407 ArgHisGlyThrMetAlaAsnAlaLeuProHis 417
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Scoring table: IDENTITY NUC
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Searched: 4300275 seqs, 287294193 residues

Total number of hits satisfying chosen parameters: 8600550

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
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c 2	3248	100.0	3309400	9 US-09-738-626-1	Sequence 1, Appli
c 3	2160	66.5	2160 9	US-09-965-825-1	Sequence 1, Appli
4	2160	66.5	2160	15 US-10-143-856-3	Sequence 3, Appli
5	2160	66.5	2160	15 US-10-078-167-4	Sequence 4, Appli
6	2160	66.5	2160	15 US-10-336-049-4	Sequence 4, Appli
7	2160	66.5	2160	15 US-10-091-342-4	Sequence 4, Appli
8	2160	66.5	2160	16 US-10-686-736-4	Sequence 4, Appl
9	1860	57.3	1860	17 US-10-781-014-85	Sequence 85, Appl
10	1860	57.3	1860	17 US-10-781-014-85	Sequence 85, Appl
11	944	29.1	944	17 US-10-781-014-89	Sequence 89, Appl
12	875	26.9	875	9 US-09-965-825-4	Sequence 3, Appl1
13	875	26.9	875	15 US-10-143-856-5	Sequence 5, Appli
14	875	26.9	875	15 US-10-078-167-6	Sequence 6, Appli
15	875	26.9	875	15 US-10-336-049-6	Sequence 6, Appli
16	875	26.9	875	15 US-10-091-342-6	Sequence 6, Appli
17	822	25.3	875	16 US-10-686-736-6	Sequence 6, Appli
18	813.8	25.1	1140	9 US-09-738-626-2872	Sequence 2872, Ap
19	721.4	22.2	1734	16 US-10-282-122A-17635	Sequence 17635, A
20	721.4	22.2	1422	9 US-09-965-825-12	Sequence 12, Appl
21	613	18.9	613	9 US-09-965-825-7	Sequence 7, Appli
22	613	18.9	552	17 US-10-781-014-87	Sequence 87, Appli
c 23	523	17.0	552	17 US-10-156-761-1	Sequence 1, Appli
24	522.6	16.1	9025608	15 US-10-156-761-2067	Sequence 2067, Ap
25	475	14.6	475	9 US-09-965-825-6	Sequence 6, Appli
26	397.6	12.2	1710	15 US-10-369-493-39295	Sequence 39295, A
27	397.6	12.2	1710	15 US-10-369-493-39670	Sequence 39670, A
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29	381	11.7	1737	15 US-10-282-122A-12285	Sequence 12285, A
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33	363.2	11.2	1728	16 US-10-282-122A-14452	Sequence 14452, A
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37	345.2	10.6	1806	16 US-10-282-122A-13519	Sequence 13519, A
38	344.8	10.6	1719	9 US-09-815-242-9898	Sequence 9898, A
39	344.8	10.6	1719	16 US-10-282-122A-39776	Sequence 39776, A
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43	305.2	9.4	1719	14 US-10-076-416-1	Sequence 1, Appli
44	305.2	9.4	1719	16 US-10-282-122A-20313	Sequence 20313, A
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-965-825-4
Sequence 4, Application US/09965825
; Patent No. US20020150999A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Hermann
; APPLICANT: THIRBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID US
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; FILE REFERENCE: 21354US0X
; CURRENT APPLICATION NUMBER: US/09/965,825
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR APPLICATION NUMBER: 2000-09-30
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 4
; LENGTH: 3248
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (802)..(2538)
; OTHER INFORMATION:
US-09-965-825-4

Query Match   100.0%;   Score 3248;   DB 9;   Length 3248;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 3248;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      241 TTGTCTACACCGATCAGAAAGAGACCACCGCTGATAACGGCGAGGAAAGCCCAACGTTGG 300
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Qy      601 TTCGACGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGAAATCCCAAAAGTGGGCA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTCGACGGGCTGAAACCAAACCAGACTGCCCAGCAACGACGGAAATCCCAAAAGTGGGCA 660

Qy      661 TCCCTGTTTGGTACCGAGTACCCACCCGGGCCTGAAACTCCCTGGCAGGCGGGCGAAGCG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TCCCTGTTTGGTACCGAGTACCCACCCGGGCCTGAAACTCCCTGGCAGGCGGGCGAAGCG 720

Qy      721 TGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACACAATAG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGGCAACAACTGGAATTTAAGAGCACAATTGAAGTCGCACCAAGTTAGGCAACACAATAG 780

Qy      781 CCATAACGTTGAGGAGTTCAGATGGCACACAGCTACGCAGAACAATTAATTGACACTTTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCATAACGTTGAGGAGTTCAGATGGCACACAGCTACGCAGAACAATTAATTGACACTTTG 840

Qy      841 GAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGTGGGTGACAGCCTTAATCCGATCGTG 900

Qy      901 GATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCG 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GATGCTGTCCGCCAATCAGATATTGAGTGGGTGCACGTTCGAAATGAGGAAGCGGCGGCG 960

Qy      961 TTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTTCTTGT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TTTGCAGCCGGTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTATGTGCTGCTTCTTGT 1020

Qy     1021 GGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTGCGAAG 1080

Qy     1081 GTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCCAGGAA 1140

Qy     1141 ACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGT 1200
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Db     1141 ACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATGGTGGT 1200

Qy     1201 GAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAGGTGTG 1260

Qy     1261 TCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTTATTCC 1320

Qy     1321 AATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCAGCG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTGCAGCG 1380

Qy     1381 CTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCGTGAAG 1440

Qy     1441 AATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCG 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 AATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGCATGCG 1500

Qy     1501 CTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTGGCCTG 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 CTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTGGCCTG 1560

Qy     1561 CTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTATTGGGT 1620
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Db     1561 CTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTATTGGGT 1620

Qy     1621 ACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAAC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 ACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATATCAAC 1680

Qy     1681 GGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCA 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 GGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTGCTGCA 1740

Qy     1741 ACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGG 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 ACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGG 1800

Qy     1801 ATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTC 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 ATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATAACGTC 1860

Qy     1861 GAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGAT 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 GAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGGCGGAT 1920

Qy     1921 AAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGTACATC 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 AAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGTACATC 1980

Qy     1981 GAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGGCTAAT 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 GAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGGCTAAT 2040

Qy     2041 GCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATG 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 GCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCGCGATG 2100

Qy     2101 TGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAA 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 TGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGCACCAA 2160

Qy     2161 CTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATG 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 CTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGGAGATG 2220
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RESULT 2
US-09-738-626-1/c
; Sequence 1; Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match   100.0%;   Score 3248;   DB 9;   Length 3309400;
Best Local Similarity   100.0%;   Pred. No. 0;   Mismatches 0;   Indels 0;   Gaps 0;
Matches 3248;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 ... 60
Db   2779305 ... 2779246

Qy   61 ... 120
Db   2779245 ... 2779186

Qy   121 ... 180
Db   2779185 ... 2779126

Qy   181 ... 240
Db   2779125 ... 2779066

Qy   241 ... 300
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Qy   301 ... 360
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Qy   481 ... 540
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Qy   2221 ... 2280
Db   2221 ... 2280

Qy   2281 ... 2340
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Qy   2341 ... 2400
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Db   2821 ... 2880

Qy   2881 ... 2940
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Qy   2941 ... 3000
Db   2941 ... 3000

Qy   3001 ... 3060
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Qy   3061 ... 3120
Db   3061 ... 3120

Qy   3121 ... 3180
Db   3121 ... 3180

Qy   3181 ... 3240
Db   3181 ... 3240

Qy   3241 3248
Db   3241 3248

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RESULT 3
US-09-965-825-1
; Sequence 1, Application US/09965825
; Patent No. US2002015099A1
; GENERAL INFORMATION:
;  APPLICANT: DUSCH, Nicole
;  APPLICANT: THOMAS, Hermann
;  APPLICANT: THIERBACH, Georg
;  TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID U
;  TITLE OF INVENTION: CORYNEFORM BACTERIA
;  FILE REFERENCE: 21354US0X
;  CURRENT APPLICATION NUMBER: US/09/965,825
;  CURRENT FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: DE 10048604.5
;  PRIOR FILING DATE: 2000-09-30
;  PRIOR APPLICATION NUMBER: DE 10117085.8
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 2160
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (327)..(2063)
;  OTHER INFORMATION:
;  NAME/KEY: -35_signal
;  LOCATION: (227)..(232)
;  OTHER INFORMATION:
;  NAME/KEY: -10_signal
;  LOCATION: (256)..(261)
;  OTHER INFORMATION:
US-09-965-825-1
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Query Match    66.5%;  Score 2160;  DB 9;  Length 2160;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2160;  Conservative  0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy   476 TTAGAGGCGGATTCTGTGGAGGTCCACTTTTGTGGGGTCTCGGGGTCTAAATTTGGCCAGTTTT 535
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Db     1 TTAGAGCGGATTCTGTGAGGTCCACTTTTTGTGGGGTCTCGGGGTCTAAATTGGCCAGTTTT 60

Qy   536 CGAGGCGGACCAGACAGCAGGCGTGCCCACGATGGTTTAAATAGGCGGGCATCGTGT 595
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CGAGGCGGACCAGACAGCAGGCGTGCCCACGATGGTTTAAATAGGCGGGCATCGTGT 120

Qy   596 TTCGGTTTTCGACGGGCTGAAAACCAAAACCAGACTGCCCAGCAACGACGGAAAAGT 655
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTCGGTTTCGACGGGCTGAAAACCAAAACCAGACTGCCCAGCAACGACGGAAAAGT 180

Qy   656 GGGCATCCCGTGTTTTGGTACCGAGTACCCCACCCCCGGGGGTCTGAAAACTCCCTG 715
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGGCATCCCGTGTTTTGGTACCGAGTACCCCACCCCCGGGGGTCTGAAAACTCCCTG 240

Qy   716 AAGCGTGGCAACAACTGGAAATTTAAGCACAAATTGAAGTCGGCACGTTAGGCAACAC 775
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGCGTGGCAACAACTGGAAATTTAAGCACAAATTGAAGTCGGCACGTTAGGCAACAC 300

Qy   776 AATAGCCATAACGTTGAGGAGTTCAGATGGCACACACGACTACCGCAGACAAATTAAATTGACA 835
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AATAGCCATAACGTTGAGGAGTTCAGATGGCACACACGACTACCGCAGACAAATTAAATTGACA 360

Qy   836 CTTTGGAAGCTCAAGGTGTGAAGCGAATTATGGTTTGGTTTGGGTGGTGACAGCCTTAATCCGA 895
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CTTTGGAAGCTCAAGGTGTGAAGCGAATTATGGTTTGGTTTGGGTGGTGACAGCCTTAATCGA 420

Qy   896 TCGTTGGATGCTGTCCCGCCAATCAGATATTGAGTGGGGTGCACGTTCGAAAATGAGGAACGG 955
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCGTTGGATGCTGTCCCGCCAATCAGATATTGAGTGGGGTGCACGTTCGAAAATGAGGAAGCGG 480

Qy   956 CGGCGGTTTGCGACCGGGTTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTTATGCTGCTT 1015
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CGGCGGTTTGCGACCGGGTTGCGGAATCGTTGATCACTGGGGAGCTGGCAGTTATGTGCTT 540

Qy  1016 CTTGTGGTCCTGGAAACACACACCTGATTCAGGTTCTTATGATTCGGCATCGAAATGGTG 1075
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Db   541 CTTGTGGTCCTGGAAACACACACCTGATTCAGGTTCTTATGATTCGGCATCGAAATGGTG 600

Qy  1076 CGAAGGGTGTTGGCCATCGGCTAGCCATATTCCGAGTGCCCAGATTGGTTGCGACGTTCTTC 1135
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CGAAGGGTGTTGGCCATCGGCTAGCCATATTCCGAGTGCCCAGATTGGTTGCGACGTTCTTC 660

Qy  1136 AGGAAAACGGCATCCGGACATTTTGTTTAAGGAATGCTCTGGGTTACTGGGGAGGATGGTGAATG 1195
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGGAAAACGGCATCCGGACATTTTGTTTAAGGAATGCTCTGGGTTACTGGGGAGGATGGTGAATG 720

Qy  1196 GTGGTGAGCAGGTGAACGCATTTGCATCAGCGGATTCAGTCCACCATGGGCGGGGTAAAG 1255
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Db   721 GTGGTGAGCAGGTGAACGCATTTGCATCAGCGGATTCAGTCCACCATGGGCGGGGTAAAG 780

Qy  1256 GTGTGTCGGTGGTAGTGTGAATTCCGGTTGTGATATCGGTAAGGAGACGACGGACGTTACTT 1315
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GTGTGTCGGTGGTAGTGTGAATTCCGGTTGTGATATCGGTAAGGAGACGACGGACGTTACTT 840

Qy  1316 ATTCCAATTCCACTATTTCTTCTGGCACTCCCGTGGCGATCCTACTACTGGAGCCTG 1375
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 ATTCCAATTCCACTATTTCTTCTGGCACTCCCGTGGCGATCCTACTACTGGAGCCTG 900

Qy  1376 CAGCGCTGGTGGAGGCGGATTAACAACGCTAAGTCTCGTCACTTTTGTTCTGCGGGGCG 1435
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGCGCTGGTGGAGGCGGATTAACAACGCTAAGTCTCGTCACTTTTGTTCTGCGGGGCG 960

Qy  1436 TGAAGAATGCTCGCGCGCAGAGTTGGGAGTTGGAAGAATTAAATCACCGGATCGCGGGC 1495
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGAAGAATGCTCGCGCGCAGAGTTGGGAGTTGGAAGAATTAAATCACCGGATCGCGGGC 1020
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Db  2776605 GAGGGATCACCTGCGCAACCATTGGGCGAGGCGGCGGGCCGAAATTTTTGCCGGCGCCAGGTTTTTACGG 2776546
Qy     2761 ACATCTTTATTGCATATCCGCTGTATCTTAACCGATCATGCATGCAGTGCAACGCCTGAACGCGA 2820
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Db  2776545 ACATCTTTATTGCATATCCGCTGTATCTTAACCGATCATGCATGCAGTGCAACGCCTGAACGCGA 2776486

Qy     2821 TCCCCGGAGAAATTTCCATTGGCGTGGGATTCGGTAGAGATGGCACAGGGCGACGGGCGGGGTT 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2776485 TCCCCGGAGAAATTTCCATTGGCGTGGGATTCGGTAGAGATGGCACAGGGCGACGGGCGGGGTT 2776426

Qy     2881 TGCGGCGAAGAGATATCAAGGGCTCTGATTGAATTGAATGGATTCGGGCGACTCGTTAGTGAGTGGAGTCA 2940
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2776425 TGCGGCGAAGAGATATCAAGGGCTCTGATTGAATTGAATGGATTCGGGCGACTCGTTAGTGAGTGGAGTCA 2776366

Qy     2941 CGGCGACTGCTTCAGAATTGAGTCAGATCTGGGGCAGGCCACGCAGCCAGCAACGACGGAAAAGT 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2776365 CGGCGACTGCTTCAGAATTGAGTCAGATCCCGGACTCCCGCGGGCGGCAGGCCACGCAGCCAGCAACGACGGAAAAGT 2776306

Qy     3001 TGTTTACTTTTCCTGGGGCATTCTTATGGGCCCGGGCGGAAAATGGTGAGCAGCAGCAGCTGATG 3060
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Qy  3061 AGCTTCAGGCTTAAACAACAGCGTCCAGCGACTTGCTTGCTTCTTCTGGGGTT 3120
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Qy  3121 CCTCGCCGGTCTGCGGCAGTTTACAGAGACGCCAATCGATCGATAGAGATGCACAAC... 3180
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Qy  3181 TTAACGATTCCCAGCAGATCACCTCGGGAGCAGGCATGCAGCACTGAGAGAACGAGG... 3240
Db  2776186

Qy  3241 TGCTGTGCT 3248
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Db  2776065 TGCTGTGCT 2776058
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RESULT 4
US-10-143-856-3
; Sequence 3, Application US/10143856
; Publication No. US2003010901A1
; GENERAL INFORMATION:
;  APPLICANT: BURKE, KEVIN
;  APPLICANT: DUNICAN, L.K.
;  APPLICANT: McCORMACK, ASHLING
;  APPLICANT: STAPLETON, CLIONA
;  APPLICANT: MOCKEL, BETTINA
;  APPLICANT: THIERBACH, GEORG
;  TITLE OF INVENTION: Process for the fermentative preparation of
;  TITLE OF INVENTION: with amplification of the tkt gene
;  FILE REFERENCE: MAS//021123/282432
;  CURRENT APPLICATION NUMBER: US/10/143,856
;  CURRENT FILING DATE:  2002-05-14
;  PRIOR APPLICATION NUMBER: 09/986,649
;  PRIOR FILING DATE:  17-03-2000
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 3
;  LENGTH: 2160
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (327)..(2063)
;  OTHER INFORMATION: poxB
US-10-143-856-3

Query Match             66.5%;   Score 2160;   DB 15;   Length 2160;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[Alignment block — Query (Qy) and Database (Db) nucleotide sequences with match bars]

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Qy       1016 CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG 1075
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Db        541 CTTGTGGTCCTGGAAACACACACCTGATTCAGGGTCTTTATGATTCGCATCGAAATGGTG 600

Qy       1076 CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCC 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAAGGTGTTGGCCATCGCTAGCCATATTCCGAGTGCCCAGATTGGTTCGACGTTCTTCC 660

Qy       1136 AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGAAACGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTGCGAGATGGTGAATG 720

Qy       1196 GTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAG 1255
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Db        721 GTGGTGAGCAGGGTGAACGCATTTTGCATCACGCGATTCAGTCCACCATGGCGGGTAAAG 780

Qy       1256 GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTT 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTGTGTCGGTGGTAGTGATTCCTGGTGATATCGCTAAGGAAGACGCAGGTGACGGTACTT 840

Qy       1316 ATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTG 1375
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Db        841 ATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCGGATCCTACTGAGGCTG 900

Qy       1376 CAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCG 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGCGCTGGTGGAGGCGATTAACAACGCTAAGTCTGTCACTTTGTTCTGCGGTGCGGGCG 960

Qy       1436 TGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGC 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGAAGAATGCTCGCGCGCAGGTGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGC 1020

Qy       1496 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG 1555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGCGCTGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTTGAGGTCGGCATGTCTG 1080

Qy       1556 GCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTAT 1615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCTGCTTGGTTACGGCGCCTGCGTGGATGCGTCCAATGAGGCGGATCTGCTGATTCTAT 1140

Qy       1616 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATA 1675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGGGTACGGATTTCCCTTATTCTGATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGATA 1200

Qy       1676 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTG 1735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCAACGGTGCGCACATTGGTCGACGTACCACGGTGAAGTATCCGGTGACCGGTGATGTTG 1260

Qy       1736 CTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTG 1795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTG 1320

Qy       1796 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATA 1855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATCGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATA 1380

Qy       1856 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG 1915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCTATTTTGAACGAGCTGG 1440

Qy       1916 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGT 1975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGGATAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCGAGGT 1500

Qy       1976 ACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGG 2035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTCCGCCACGGCACGATGG 1560

Qy       2036 CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG 2095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTAATGCGTTGCCTCATGCGATTGGTGCGCAAAGTGTTGATCGAAACCGCCAGGTGATCG 1620

Qy       2096 CGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC 2155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CGATGTGTGGCGATGGTGGTTTGGGCATGCTGCTGGGTGAGCTTCTGACCGTTAAGCTGC 1680

Qy       2156 ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 2215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACCAACTTCCGCTGAAGGCTGTGGTGTTTAACAACAGTTCTTTGGGCATGGTGAAGTTGG 1740

Qy       2216 AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG 2275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AGATGCTCGTGGAGGGACAGCCAGAATTTGGTACTGACCATGAGGAAGTGAATTTCGCAG 1800

Qy       2276 AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCG 2335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AGATTGCGGCGGCTGCGGGTATCAAATCGGTACGCATCACCGATCCGAAGAAAGTTCGCG 1860

Qy       2336 AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATC 2395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGATATCGTCACGGATC 1920

Qy       2396 CTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGG 2455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTAATGCGCTGTCGATCCCACCAACCATCACGTGGGAACAGGTCATGGGATTCAGCAAGG 1980

Qy       2456 CGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGATCTGGCCCGTTCGA 2515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CGGCCACCCGAACCGTCTTTGGTGGAGGAGTAGGAGCGATGATCGATCTGGCCCGTTCGA 2040

Qy       2516 ACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTTCTCATTGACCGCGA 2575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTTCTCATTGACCGCGA 2100

Qy       2576 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT 2635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACGCCGGTGCCCATGAGATTGCCCT 2160

RESULT 5
US-10-078-167-4
; Sequence 4, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
;  APPLICANT: Dunican, Rita
;  APPLICANT:  McCormack, Ashling
;  APPLICANT:  Stapleton, Cliona
;  APPLICANT:  Burke, Kevin
;  APPLICANT:  Mockel, Bettina
;  TITLE OF INVENTION: Process for the preparation of L-amino acids using
;  TITLE OF INVENTION:  a gene encoding 6-Phosphogluconate Dehydrogenase
;  FILE REFERENCE: 990229 BT-US-B
;  CURRENT APPLICATION NUMBER: US/10/078,167
;  CURRENT FILING DATE:  2002-02-20
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2160
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (327)..(2063)
;   OTHER INFORMATION: poxB
US-10-078-167-4

  Query Match             66.5%;  Score 2160;  DB 15;  Length 2160;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2160;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        476 TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAGAGGCGATTCTGTGAGGTCACTTTTTGTGGGGTCGGGGTCTAAATTTGGCCAGTTTT 60

Qy        536 CGAGGCGACCAGACAGGCGTGCCCACGATGTTTAAATAGGCGATCGGTGGGCATCTGTGT 595
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Db   61 CGAGGCGACCAGACAGGCGTGCCCACGATGTGTTAAATAGGCGGATGGGTGGGCATCTGTGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   596 TTGGTTTCGACGGGGCTGAAACCAACAGACTGCCCCAGCAACCAGACAGACGGAAATCCCAAAGT 655
Db   121 TTGGTTTCGACGGGGCTGAAACCAACAGACTGCCCCAGCAACCAGACAGACGGAAATCCCAAAGT 180

Qy   656 GGGCATCCCTGTTTCGTTACCCGAGTACCCAGTACCACCGGTACCTGCCAGGGGGGG 715
Db   181 GGGCATCCCTGTTTCGTTACCCGAGTACCCAGTACCACCGGTACCTGCCAGGGGGGG 240

Qy   776 AATAGCCAATAACGTTGAGGAGTTCAGATGGCCACAGAACAATTAATTGACA 835
Db   301 AATAGCCAATAACGTTGAGGAGTTCAGATGGCCACAGAACAATTAATTGACA 360

... (DNA sequence alignment, Qy/Db pairs continue) ...

Qy 1616 TGGGTACGGATTTCCCTTATTCTGAATTTCCTTCCTAAAGACAACGTTGCCCAGGTGGGATA 1675
Db 1616 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 2101 GCGCTTAACTGCCAACATTTCCAGGATGGCAGCTCACCGCGGTGGCCCATGAGAGATTGCCCT 2160

```
;  APPLICANT:  Bathe, Brigitte
;  APPLICANT:  Reth, Alexander
;  APPLICANT:  Thierbach, Georg
;  APPLICANT:  Kreutzer, Caroline
;  APPLICANT:  Mockel, Bettina
;  TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification o
;  TITLE OF INVENTION: the zwf Gene
;  FILE REFERENCE: 7601/80158
;  CURRENT APPLICATION NUMBER: US/10/336,049
;  CURRENT FILING DATE: 2003-01-30
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: Patentin version 3.1
;
;  SEQ ID NO 4
;  LENGTH: 2160
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (327)..(2063)
;  OTHER INFORMATION: poxB

US-10-336-049-4

  Query Match             100.0%;  Score 2160;  DB 15;  Length 2160;
  Best Local Similarity   100.0%;
  Matches 2160;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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(Alignment blocks of query (Qy) vs database (Db) DNA sequence follow, spanning positions 1–2160, all identically matched. Representative block position markers are shown below.)

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Qy    476  ...  535
Db      1  ...   60
Qy    536  ...  595
Db     61  ...  120
Qy    596  ...  655
Db    121  ...  180
Qy    656  ...  715
Db    181  ...  240
Qy    716  ...  775
Db    241  ...  300
Qy    776  ...  835
Db    301  ...  360
Qy    836  ...  895
Db    361  ...  420
Qy    896  ...  955
Db    421  ...  480
Qy    956  ... 1015
Db    481  ...  540
Qy   1016  ... 1075
Db    541  ...  600
Qy   1076  ... 1135
Db    601  ...  660
Qy   1136  ... 1195
Db    661  ...  720

Qy   1196  ... 1255
Db    721  ...  780
Qy   1256  ... 1315
Db    781  ...  840
Qy   1316  ... 1375
Db    841  ...  900
Qy   1376  ... 1435
Db    901  ...  960
Qy   1436  ... 1495
Db    961  ... 1020
Qy   1496  ... 1555
Db   1021  ... 1080
Qy   1556  ... 1615
Db   1081  ... 1140
Qy   1616  ... 1675
Db   1141  ... 1200
Qy   1676  ... 1735
Db   1201  ... 1260
Qy   1736  ... 1795
Db   1261  ... 1320
Qy   1796  ... 1855
Db   1321  ... 1380
Qy   1856  ... 1915
Db   1381  ... 1440
Qy   1916  ... 1975
Db   1441  ... 1500
Qy   1976  ... 2035
Db   1501  ... 1560
Qy   2036  ... 2095
Db   1561  ... 1620
Qy   2096  ... 2155
Db   1621  ... 1680
Qy   2156  ... 2215
Db   1681  ... 1740
Qy   2216  ... 2275
Db   1741  ... 1800
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Qy   2276 AGAATTGCGGGGGCCTCGCGGGTTATCAAATCGGTTACGGCATCCGGATCCGGATCACCGAGAAAAGTTCGCG 2335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGAATTGCGGGGGCCTCGCGGGTTATCAAATCGGTTACGGCATCCGGATCCGGATCACCGAGAAAAGTTCGCG 1860

Qy   2336 AGCAGCTAGCTGAGCGCATTGGCATATATCCTTGGACATCGTACTGATCGATAATCGTCACGGATC 2395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGCAGCTAGCTGAGCGCATTGGCATAATCCTTGGACATCGTACTGATCGATAATCGTCACGGATC 1920

Qy   2396 CTAATGCGCTGTCGATCCCACCAACATCACGTGGGAACAGGTCATGGGATTCAGCAAGG 2455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTAATGCGCTGTCGATCCCACCAACATCACGTGGGAACAGGTCATGGGATTCAGCAAGG 1980

Qy   2456 CGGGCCACCCGAAACCGTCTTCTTTGGGTGGAGGTAGGAGGAGGCGATGATCGATCTGGCCCCGTTCGA 2515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGGCCACCCGAAACCGTCTTCTTTGGGTGGAGGTAGGAGGAGGCGATGATCGATCTGGCCCCGTTCGA 2040

Qy   2516 ACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTTCTCATTGACCGGCGA 2575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ACATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTTCTCATTGACCGGCGA 2100

Qy   2576 GCGCTTAACTGCCAACATTTCAGGATGGCAGCTCACGCCCGGTGCCCATGAGATTGCCCCT 2635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GCGCTTAACTGCCAACATTTCAGGATGGCAGCTCACGCCCGGTGCCCATGAGATTGCCCCT 2160
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RESULT 7
US-10-091-342-4
; Sequence 4, Application US/10091342
; Publication No. US20030190045A1
; GENERAL INFORMATION:
;   APPLICANT: National University of Ireland, Galway
;   APPLICANT: Degussa AG
;   APPLICANT: Forschungszentrum Julich GmbH
;   TITLE OF INVENTION: Process for the fermentative Preparation of L-Amino Acids with
;   TITLE OF INVENTION: Amplification of the zwf Gene.
;   FILE REFERENCE: 990239BT
;   CURRENT APPLICATION NUMBER: US/10/091,342
;   CURRENT FILING DATE: 2002-03-06
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 4
;   LENGTH: 2160
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (327)..(2063)
;   OTHER INFORMATION: poxB
US-10-091-342-4

Query Match   66.5%; Score 2160; DB 15; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    476 TTAGAGGCGATTCGTGAGGTCACTTTTTGTGGGGTGGGGTCGGGGTCGGGGGTCTAAATTTGGGAGTTTTT 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTAGAGGCGATTCGTGAGGTCACTTTTTGTGGGGTGGGGTCGGGGTCTAAATTTGGCCCAGTTTT 60

Qy    536 CGAGGCGACGACAGGGCTGCCCACGACTTTTGGGGGTGGGGCATCTGTGT 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGAGGCGACGACAGGGCTGCCCACGATGTTTAAATAGGCGACTCGTGATGGCCAGTGTCT 120

Qy    596 TTGGTTTCGACGGGCTGAAACCAAGACAAGCAGAGAGGAAATCCCAAAAGT 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTGGTTTCGACGGGCTGAAACCAAGACAAGCAGAGAGGAAATCCCAAAAGT 180

Qy    656 GGGCCATCCCTGTTTGGGTACCGAGTACCACCCGGGCGGGAAATCCCAAAAGT 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGGCATCCCTGTTTGGGTACCGAGTACCACCCGGGCGGGGGCG 240

Qy    716 AAGGCGTGGCAACAACTGGAATTTAAGAGAGCACAATTGAAGTCGGCACCAAGTTAGGCGAACAC 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGGCTGGGCAACAACTGGAATTTAAGAGAGCACAATTGAAGTCGGCACCAAGTTAGGCGAACAC 300

Qy    776 AATAGCCATAACGTTGAGGAGTTCAGATGTGGCACACAGCCTAGCGCAGAACAATTAATTGACA 835
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AATAGCCATAACGTTGAGGAGTTCAGATGTGGCACACAGCCTAGCGCAGAACAATTAATTGACA 360

Qy    836 CTTTGGAAGCTCAAGTGTGAAGGCGAAATTTATGGTTTGGTGGTGACAGCCTTAATCCGA 895
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTTTGGAAGCTCAAGTGTGAAGGCGAAATTTATGGTTTGGTGGTGACAGCCTTAATCCGA 420

Qy    896 TCGTGGAATGCTGTCCGCCAATCAGATATTGAGTGGTGTGCACGTTCGAAAATGAGGAAGCGG 955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCGTGGAATGCTGTCCGCCAATCAGATATTGAGTGGTGTGCACGTTCGAAAATGAGGAAGCGG 480

Qy    956 CGGCGTTTGCAGCCGGTGCGGAAATCGTTGATCACTGGGGAGCTGGCAGTGTCGCTT 1015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGGCGTTTGCAGCCGGTGCGGAAATCGTTGATCACTGGGGAGCTGGCAGTGTCGCTT 540

Qy   1016 CTTGTCGGTCCTTGGAAACACACACCTGATTCAGGGTCTTTATGATCGGATCGAAATCGGTG 1075
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTTGTCGGTCCTTGGAAACACACACCTGATTCAGGGTCTTTATGATCGGATCGAAATCGGTG 600

Qy   1076 CGAAGGTGTTGGGCCATCGCTAGCCATATTCCGAGTGGCCCAGAATTGGTTCGACGTTCTTCC 1135
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAAGGTGTTGGGCCATCGCTAGCCATATTCCGAGTGGCCCAGAATTGGTTCGACGTTCTTCC 660

Qy   1136 AGGAAAACGCATCCCGAGAGATTTTGTTTAAGGAAATGCTCTGGTTACTGCGAGATGGTGAATG 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGAAAACGCATCCCGAGAGATTTTGTTTAAGGAAATGCTCTGGTTACTGCGAGATGGTGAATG 720

Qy   1196 GTGGGTGAGCAGGGTGAACGGCACATTTTGCATCACGCGAGTTCAGTCGTCCACCATGCGCGGGTAAAG 1255
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGGGTGAGCAGGGTGAACGGCACATTTTGCATCACGCGAGTTCAGTCGTCCACCATGCGCGGGTAAAG 780

Qy   1256 GTGGTGTCGGTGGTAGTGATTCCTGGTGATGATCGCTAAAGGAAGAGACGGCAGGTGACGGTACTT 1315
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGTTGTCGGTGGTAGTGATTCCTGGTGATGATCGCTAAAGGAAGAGACGGCAGGTGACGGTACTT 840

Qy   1316 ATTCCAATTCCACTATTTCTTCTTCTGGCACTCCTGTGGTTCCCGGATCCTTACTGAGGCTG 1375
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATTCCAATTCCACTATTTCTTCTTCTGGCACTCCTGTGGTTCCCGGATCCTTACTGAGGCTG 900

Qy   1376 CAGCCGCTGGTGGAGCGGATTAACAACGGCTAAGTCTGTCACTTTGTTCTGGGTGCGGGCG 1435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGCCGCTGGTGGAGCGGATTAACAACGGCTAAGTCTGTCACTTTGTTCTGGGTGCGGGCG 960

Qy   1436 TGAAGAAATGCTCGCCGCGACGTGTTGGAGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGGC 1495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGAAGAAATGCTCGCCGCGACGTGTTGGAGTTGGAGTTGGCGGAGAAGATTAAATCACCGATCGGGC 1020

Qy   1496 ATGCGCTGGCTGGGTAAGCACGTACATCCAGCATGAGAATCCGTTTGAGGTGTCGGCAAGTCTG 1555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGCGCTGGGTGGGTAAGCACTACATCCAGCATGAGAATCCGTTTGAGGTGTCGGCCAGTGTCG 1080

Qy   1556 GCCTGCTTGGTTACGGCGCCTGCGCTGGCAATGGCTCCAATGAGGCGGGATCTGCTGATTCTAT 1615
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCCTGCTTGGTTACGGCGCCTGCGCTGGCAATGGCTCCAATGAGGCGGGATCTGCTGATTCTAT 1140

Qy   1616 TGGGTACGGGGATTTCCCTTTATTCTGATTTCCTTCCTTCCTAAAGAGAACACGTTGCCCAGTGGGGATA 1675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGGGTACGGGGATTTCCCTTTATTCTGATTTCCTTCCTTCCTAAAGAGAACACGTTGCCCAGTGGGGATA 1200

Qy   1676 TCAACGGGTGCGCACATTGGTCGACCTACCACGGGTGAAGTATCCGTGACCGGTGATGTTG 1735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCAACGGGTGCGCACATTGGTCGACCTACCACGGGTGAAGTATCCGTGACCGGTGATGTTG 1260

Qy   1736 CTGCAACGAATGAAAATATTTTGCCTCATGTGAAGGAAGGAAAAAACAGATGTCCTTCCTTG 1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 CTGCAACGAATGAAAATATTTTGCCTCATGTGAAGGAAGGAAAAAACAGATCGTTCCTTG 1320

Qy   1796 ATCGGATGCTCAAGGCACGACGAGCGTAAGTTGAGCTGGTCGGTTAGAGACGTACACATA 1855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCGGATGCTCAAGGCACGACGAGCGTAAGTTGAGCTGGTCGGTTAGAGACGTACACATA 1380
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; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxB
US-10-686-736-4

Query Match   66.5%; Score 2160; DB 16; Length 2160;
Best Local Similarity   100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    476 TTAGAGGCGATTCTTGTGAGGTCACTTTTTTGTGGGGTTCTAAATTTTGGCCAGTTTT 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTAGAGGCGATTCTTGTGAGGTCACTTTTTTGTGGGGTTCTAAATTTTGGCCAGTTTT  60

Qy    536 CGAGGCGACCAGAACAGGCGTGCCCACGANGTTTAAATAGGCGATCGGTGGGGCATCTGT 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGAGGCGACCAGAACAGGCGTGCCCACGANGTTTAAATAGGCGATCGGTGGGGCATCTGT 120

Qy    596 TTGGTTTCGACGGGCGTGAAAACCAAACCAGAGTGGGGTTCGGGGGTCGGGGTTCGTCT 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TTGGTTTCGACGGGCGTGAAAACCAAACCAGAGTGGGGTTCGGGGGTCGGGGTTCGTCT 180

Qy    656 GGGCCATCCCTGTTTTGGTACCCGAGTACCCACCCGGGGGCTGAAACTCCCTGGCGGGCG 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGCCATCCCTGTTTTGGTACCCGAGTACCCACCCGGGGGCTGAAACTCCCTGGCGGGCG 240

Qy    716 AAGCGTGGCAACAACTGGAATTTAAGAGCACAGCTAGCGCAGAACAATTAATTGACA 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGCGTGGCAACAACTGGAATTTAAGAGCACAGCTAGCGCAGAACAATTAATTGACAC 300

Qy    776 AATAGCCATAAGGTTGAGGAGTTCAGATGGCACAGCTACGCAGAACAATTAATTGACA 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AATAGCCATAAGGTTGAGGAGTTCAGATGGCACACCAGCAGAACAATTAATTGACA 360

Qy    836 CTTTGGAAGCTCAAGGTGTGAAGCGGAATTTAATGGTTTGGTTCGGGTGACAGCCTTAAT 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTTTGGAAGCTCAAGGTGTGAAGCGGAATTTAATGGTTTGGTTCGGGTGACAGCCTTAAT 420

Qy    896 TCGTGGAATGCGTCCGCCAATCAGATATTGAGTGGTGGGTGCAGTTCGAAATGAGGAAGCGG 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCGTGGAATGCGTCCGCCAATCAGATATTGAGTGGTGGGTGCAGTTCGAAATGAGGAAGCGG 480

Qy    956 CGGGCGTTTGCAGCCGGTGCGGAAATCGTTGATCACTCGGCGAGCTGGCAGTGTGCTGCTT 1015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGGGCGTTTGCAGCCGGTGCGGAAATCGTTGATCACTCGGCGAGCTGGCAGTGTGCTGCTT 540

Qy   1016 CTTGTGGTGGTTCCTGGAAACACACACCTGAATTCAGGGGTCTTTATGAGTTCCATCGAAATGGTG 1075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTTGTGGTGGTTCCTGGAAACACACACCTGAATTCAGGGGTCTTTATGAGTTCCATCGAAATGGTG 600

Qy   1076 CGAAGGTGTTGGCCATCGCTAGCCATATTCCCAGTGCCCAGATTGGTTCGACGGTTCTTCC 1135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAAGGTGTTGGCCATCGCTAGCCATATTCCCAGTGCCCAGATTGGTTCGACGGTTCTTCC 660

Qy   1136 AGGAAACGGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTCGGAGGATGGAATG 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGGAAACGGCATCCGGAGATTTTGTTTAAGGAATGCTCTGGTTACTCGGAGGATGGAATG 720

Qy   1196 GTGGTGAGCAGGGTGAACGCATTTGCATCACGCGGATCCACCATGGGGGGTAAAG 1255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGGTGAGCAGGGTGAACGCATTTGCATCACGCGGATCCACCATGGGGGGTAAAG 780

Qy   1256 CTGTGTCGGTGGTAGTGAATTCCTGGTGATATCGCTAAGGAGAGACGGGACGGTACTT 1315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGTGTCGGTGGTAGTGAATTCCTGGTGATATCGCTAAGGAGAGACGGGACGGTACTT 840

Qy   1316 ATTCCAAATTCCACTATTTCTTCTGCGACTCCTGTTCCCGGATCCTACTGAGGCTG 1375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATTCCAAATTCCACTATTTCTTCTGCGACTCCTGTTCCCGGATCCTACTGAGGCTG 900
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Qy   1856 ACGTCGAGAAGCANTGCCTATTCACCCTGAAATACGTTGCCTCTATTTGAAACGAGCTGG 1915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACGTCGAGAAGCANTGCCTATTCACCCTGAAATACGTTGCCTCTATTTGAAACGAGCTGG 1440

Qy   1916 CGGATAAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCAGGT 1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CGGATAAAGGATGCGGTGTTTACTGTGGATACCGGCATGTGCAATGTGTGGCATGCAGGT 1500

Qy   1976 ACATCGAGAATCCGGAGGGAACGCGGCGACTTTGTGGGTTCATTCCGGCCACGGACGATGG 2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACATCGAGAATCCGGAGGGAACGCGGCGACTTTGTGGGTTCATTCCGGCCACGGACGATGG 1560

Qy   2036 CTAATGCGTTGCCTCATGCGGATTGGTGCGCGAAAGTGTTGAAACCGCCACGGTGATCG 2095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CTAATGCGTTGCCTCATGCGGATTGGTGCGCGAAAGTGTTGAAACCGCCACGGTGATCG 1620

Qy   2096 CGGATGTGTGGCGATGGTGGTTGTTGGGGTGAGCTTCTGACCGTTAAGCTGC 2155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CGGATGTGTGGCGATGGTGGTTGTTGGGGTGAGCTTCTGACCGTTAAGCTGC 1680

Qy   2156 ACCAACTTCCGCTGAAAGGCTGTGGTGTTTAACACAGTTCTTTGGCATGGTGAAGTTGG 2215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACCAACTTCCGCTGAAAGGCTGTGGTGTTTAACACAGTTCTTTGGCATGGTGAAGTTGG 1740

Qy   2216 AGATGCTTCGTGGAGGGACAGCCAGAATTGGTACTGACCATGAATGGGTGAAATTCGCAG 2275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGATGCTTCGTGGAGGGACAGCCAGAATTGGTACTGACCATGAATGGGTGAAATTCGCAG 1800

Qy   2276 AGAATTGGCGCGGGCTGCGGGGTATCAAATCGTACGCATCACCGATCGGAAGAAAGTTCGCG 2335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGATTGGCGCGGGCTGCGGGGTATCAAATCGTACGCATCACCGATCGGAAGAAAGTTCGCG 1860

Qy   2336 AGCACTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGGTCACGGACGGATC 2395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGCAGCTAGCTGAGGCATTGGCATATCCTGGACCTGTACTGATCGGTCACGGACGGATC 1920

Qy   2396 CTAATGCGTGTCGATCCCACCAACCATCACGTGGGAACAGGTGACAGGTGATCACGCAAGG 2455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTAATGCGTGTCGATCCCACCAACCATCACGTGGGAACAGGTGACAGGTGATCACGCAAGG 1980

Qy   2456 CGGCCACCCGAACCGTCTCTTTGGTGGAAGGAGTAGGAGCGAGGAATCGGATCGGCCCCGTTCGA 2515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CGGCCACCCGAACCGTCTCTTTGGTGGAAGGAGTAGGAGCGAGGAATCGGATCTGGCCCCGTTCGA 2040

Qy   2516 ACATAAGGAATATTCCTACTCCATGATGATGACGACTGCGTCGTTCTCTCATTGACCGGCGA 2575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ACATAAGGAATATTCCTACTCCATGATGATGACGACTGCGTCGTTCTCATTGACCGGCGA 2100

Qy   2576 GCGCTTAACTGCCAACATTTCCAGATGGCAGCTCACGCCGGTGCCCATGAGAGATTGCCCT 2635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GCGCTTAACTGCCAACATTTCCAGATGGCAGCTCACGCCGGTGCCCATGAGAGATTGCCCT 2160
```

RESULT 9
US-10-781-014-85

; Sequence 85, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: BGI-1226CPCN
; CURRENT APPLICATION NUMBER: US/10/781,014
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 09/602,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/143,208
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/151,572
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931412.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931424.1
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931428.4
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 85
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1837)
; OTHER INFORMATION: RXN00635

US-10-781-014-85

Query Match   57.3%;   Score 1860;   DB 17;   Length 1860;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1860;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   702   CTGGCAGGGCGGCGGGCCGAAGCGTGGCAACAACTGGAATTGGAAGTCGCACC   761
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   CTGGCAGGGCGGCGGGCCGAAGCGTGGCAACAACTGGAATTGGAAGTCGCAC   60

Qy   762   AAGTTAGGCAACACAATAGCCATAACGTTGAGGAGTTCAGATGGCACACAGCTACGCAGA   821
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   AAGTTAGGCAACACAATAGCCATAACGTTGAGGAGTTCAGATGGCACACAGCTACGCAGA   120

Qy   822   ACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGAATTTATGGTTTGGGTGGGTGA   881

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(DNA sequence alignment — Qy (query) / Db (database) pairs with match lines, positions 121 through 2873)
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RESULT 10
US-09-738-626-2873
; Sequence 2873, Application US/09738626
; Publication No. US2002019760SA1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2873
; LENGTH: 1737
; TYPE: DNA

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;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-2873

Query Match     53.5%;  Score 1737;  DB 9;  Length 1737;
Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches  0;
Matches 1737;  Conservative   0;  Indels   0;  Gaps   0;

Qy    802 ATGGCACAGCTAGCCGAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 861
Db      1 ATGGCACAGCTAGCCGAGAACAATTAATTGACACTTTGGAAGCTCAAGGTGTGAAGCGA 60

Qy    862 ATTTATTGGTTTGGTCGGGTGACAGCCTTAATCGATCGGATGGTTCCGCCCAATCAGAT 921
Db     61 ATTTATTGGTTTGGTCGGGTGACAGCCTTAATCGATCGGATGGTTCCGCCCAATCAGAT 120

Qy    922 ATTGAGTGGGGTGCACGTTCGAAAATGAGGAAGCGGGGCGTGCCGAAATCG 981
Db    121 ATTGAGTGGGGTGCACGTTCGAAAATGAGGAAGCGGGGCGTGCCGAAATCG 180

Qy    982 TTGATCACTCGGGAGCTGGGCAGTAGTGCTGGTCGTCGGATGGGTTGCAGCCGGTTGGGGC 1041
Db    181 TTGATCACTCGGGAGCTGGGCAGTAGTGCTGGTCGTCGGATGGGTTGCAGCCGGTTGGGGC 240

Qy   1042 ATTCAGGGGTCTTTATGAGTTCGCATCGGAAAATGGTGGGGAGGTGTTGGGCATGCCTAGCCAT 1101
Db    241 ATTCAGGGGTCTTTATGAGTTCGCATCGGAAAATGGTGGGGAGGTGTTGGGCATGCCTAGCCAT 300

Qy   1102 ATTCCGAGTTGCCCAGATTGGTTCGACGTTCTTCCAGGAAAACGCATCCGAGAGATTTGTTT 1161
Db    301 ATTCCGAGTTGCCCAGATTGGTTCGACGTTCTTCCAGGAAAACGCATCCGAGAGATTTGTTT 360

Qy   1162 AAGGAATGCTCTCGGTTACTGCCGAGATGGTGGTTGGTGGTCAGCGGTGAAACGGCATTTTG 1221
Db    361 AAGGAATGCTCTCGGTTACTGCCGAGATGGTGGTTGGTGGTCAGCGGTGAAACGGCATTTTG 420

Qy   1222 CATCACGCGGATTCAGTCAGCAGGTGAGGGGTAAAGGTGTTCGGTGGTAGTGATTCCTGGT 1281
Db    421 CATCACGCGGATTCAGTCAGCAGGTGAGGGGTAAAGGTGTTCGGTGGTAGTGATTCCTGGT 480

Qy   1282 GATATCGCTAAGGAAGACGCGGTGACGGTACTTATTCCAATTCCACTATTCTTCTGGC 1341
Db    481 GATATCGCTAAGGAAGACGCGGTGACGGTACTTATTCCAATTCCACTATTCTTCTGGC 540

Qy   1342 ACTCCTGTGTGTTCCCGGATCCTCAGCGCCTGGTGGAGGCGGATTAAACAAC 1401
Db    541 ACTCCTGTGTGTTCCCGGATCCTCAGCGCCTGGTGGAGGCGGATTAAACAAC 600

Qy   1402 GCTAAGTCTGTCACTTTGTTCTCGCGGTGCGGGGCTGAGAAATGCTCGCGCGCAGGTGTTG 1461
Db    601 GCTAAGTCTGTCACTTTGTTCTCGCGGTGCGGGGCTGAGAAATGCTCGCGCGCAGGTGTTG 660

Qy   1462 GAGTTGGGCGGAGAAGATTAAATCACCGATACGGGCCATGCGCCTGGGGTGGGTAAGCAGTACAATC 1521
Db    661 GAGTTGGGCGGAGAAGATTAAATCACCGATACGGGCCATGCGCCTGGGGTGGGTAAGCAGTACAATC 720

Qy   1522 CAGCATGAGAATCGCTTTGAGGTCGGCAATGTCTGGCTGCCTTGGTTACGGCGGCCTGGCTG 1581
Db    721 CAGCATGAGAATCGCTTTGAGGTCGGCAATGTCTGGCTGCCTTGGTTACGGCGGCCTGGCTG 780

Qy   1582 GATGGCGTCCAAATGAGGCGGGATCTGCTGATTCGATTCCTATTGGTTCCCTTATTCTATTCTGAT 1641
Db    781 GATGGCGTCCAAATGAGGCGGGATCTGCTGATTCGATTCCTATTGGTTCCCTTATTCTATTCTGAT 840

Qy   1642 TTCCTTCCTAAAGCAACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGT 1701
Db    841 TTCCTTCCTAAAGCAACAACGTTGCCCAGGTGGATATCAACGGTGCGCACATTGGTCGACGT 900

Qy   1702 ACCACGGTGAAGTATCCGTGACCGGTGATGTGTTGCTGCAACAATCGAAAAATATTTTGCCT 1761
Db    901 ACCACGGTGAAGTATCCGTGACCGGTGATGTGTTGCTGCAACAATCGAAAAATATTTTGCCT 960

Qy   1762 CATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGGCGT 1821
Db    961 CATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGGCGT 1020

Db    961 CATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGATCGGATGCTCAAGGCACACGAGGCGT 1020

Qy   1822 AAGTTGAGCTCGGTGGTTAGAGACAGGTACAACACATAACGTCGAGAGCATGTGCCTATTCAC 1881
Db   1021 AAGTTGAGCTCGGTGGTTAGAGACAGGTACAACACATAACGTCGAGAGCATGTGCCTATTCAC 1080

Qy   1882 CCTGAATACGTTGCCTCTATTTTGAACGAGACACACATTAACGGTAAGGATGCGGGATTACTGTG 1941
Db   1081 CCTGAATACGTTGCCTCTATTTTGAACGAGACACACATTAACGGTAAGGATGCGGGATTACTGTG 1140

Qy   1942 GATACCGGCATGTGCAAGTGTGGTGGAAGGTACATCGAGAATCGGAGAATCCGGAGCGGC 2001
Db   1141 GATACCGGCATGTGCAAGTGTGGTGGAAGGTACATCGAGAATCGGAGAATCCGGAGCGGC 1200

Qy   2002 GACTTTGTGGGGTTCATTCCGCCACCAGCGCACCGATGGTCAATGCGCTTGCCTCATGCGGATTGGT 2061
Db   1201 GACTTTGTGGGGTTCATTCCGCCACCAGCGCACCGATGGTCAATGCGCTTGCCTCATGCGGATTGGT 1260

Qy   2062 GCGCAAAAGTGTTGATCGGAAACGCGCAGGTGATCCGGATGTGGTGGGCCGGATGGTGTTTGGGC 2121
Db   1261 GCGCAAAAGTGTTGATCGGAAACGCGCAGGTGATCCGGATGTGGTGGGCCGGATGGTGTTTGGGC 1320

Qy   2122 ATGCTGGCTGGGGTGGAGCTTCTGACCGTTAAGCTGCACCAACTTCGCGTGAAGGCTGTGGTG 2181
Db   1321 ATGCTGGCTGGGGTGGAGCTTCTGACCGTTAAGCTGCACCAACTTCGCGTGAAGGCTGTGGTG 1380

Qy   2182 TTTAACAACAGTTCTTTGGGGCATGGTGAAGTTGGAGATGGTCGTTGGTGGTGGAGGGACAGCCAGAA 2241
Db   1381 TTTAACAACAGTTCTTTGGGGCATGGTGAAGTTGGAGATGGTCGTTGGTGGTGGAGGGACAGCCAGAA 1440

Qy   2242 TTTGGTTACTGACCATGAGGAAGTGAAATTTCGCAGAGATTGGGAGAGTGTTATCAAA 2301
Db   1441 TTTGGTTACTGACCATGAGGAAGTGAAATTTCGCAGAGATTGGGAGAGTGTTATCAAA 1500

Qy   2302 TCGGTTACGGCATCACCGATCCGAACGAAAAGTTCGCCGAGACGCGCGGCCATTGGCATAT 2361
Db   1501 TCGGTTACGGCATCACCGATCCGAACGAAAAGTTCGCCGAGACGCGCGGCCATTGGCATAT 1560

Qy   2362 CCTGGACCTGTACTGATCGGATATCGTCACGGATCCTAATGCGCTGTCGACTGCCACCAACC 2421
Db   1561 CCTGGACCTGTACTGATCGGATATCGTCACGGATCCTAATGCGCTGTCGACTGCCACCAACC 1620

Qy   2422 ATCACGTGGGAACAGGTCATGGGATTCAGCCAAGCGGCGGCCACCCGAACCGGTCTTTTGGTGGA 2481
Db   1621 ATCACGTGGGAACAGGTCATGGGATTCAGCCAAGCGGCGGCCACCCGAACCGGTCTTTTGGTGGA 1680

Qy   2482 GGAGTAGGAGCGATGAATCGAATCTCGGCCCGGTTCGAACATAAGGAATATTCCTACTCCA 2538
Db   1681 GGAGTAGGAGCGATGAATCGAATCTCGGCCCGGTTCGAACATAAGGAATATTCCTACTCCA 1737
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RESULT 11
US-10-781-014-89
;   Sequence 89, Application US/10781014
;   Publication No. US20040180408A1
;   GENERAL INFORMATION:
;   APPLICANT: Pompejus, Markus
;   APPLICANT: Kroger, Burkhard
;   APPLICANT: Schroder, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;   TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
;   TITLE OF INVENTION: PRODUCTION
;   FILE REFERENCE: BGI-126CPCN
;   CURRENT APPLICATION NUMBER: US/10/781,014
;   CURRENT FILING DATE: 2004-02-17
;   PRIOR APPLICATION NUMBER: US 09/602,740
;   PRIOR FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: 60/141,031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 60/143,208
;   PRIOR FILING DATE: 1999-07-09

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;   PRIOR APPLICATION NUMBER: 60/151,572
;   PRIOR APPLICATION FILING DATE: 1999-08-31
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931412.8
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931413.6
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931419.5
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931420.9
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931424.1
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931428.4
;   PRIOR APPLICATION FILING DATE: 1999-07-08
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 784
;   SEQ ID NO 89
;   LENGTH: 944
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION: FRXA00635
US-10-781-014-89

Query Match      29.1%;    Score 944;   DB 17;     Length 944;
Best Local Similarity   100.0%;   Pred. No. 2e-292;
Matches  944;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;
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Qy   1618 GGTACGGGATTTCCCTTATTCTTCCTTCCTTCCTGATTTCGTTCGATTGTGCCCAGGTGGATATC 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGTACGGGATTTCCCTTATTCTTCCTTCCTTCCTGATTTCGTTCGATTGTGCCCAGGTGGATATC   60

Qy   1678 AACCGTGCCGACAATTGGTCGACGTACCACCGGTGAAGTATCCGGTGATCGGGTGATGTTGCT 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AACCGTGCCGACAATTGGTCGACGTACCACCGGTGAAGTATCCGGTGATCGGGTGATGTTGCT  120

Qy   1738 GCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGAT 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCAACAATCGAAAATATTTTGCCTCATGTGAAGGAAAAAACAGATCGTTCCTTCCTTGAT  180

Qy   1798 CGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATAAC 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGGATGCTCAAGGCACACGAGCGTAAGTTGAGCTCGGTGGTAGAGACGTACACACATAAC  240

Qy   1858 GTCCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGGCTTCCTCATTTTGAACGAGCTGGGCG 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTCCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGGCTTCCTCATTTTGAACGAGCTGGGCG  300

Qy   1918 GATAAGGATCGCGGTGTTTACTGTGATACCCGGCCATGTGCCATGCGAGGTAC 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GATAAGGATCGCGGTGTTTACTGTGATACCCGGCCATGTGCCATGCGAGGTAC  360

Qy   1978 ATCAGAAATCCGGAGGACGCGCGACTTTGTGGGTTCATTCCGCCACGCGACGATGGCT 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATCAGAAATCCGGAGGACGCGCGACTTTGTGGGTTCATTCCGCCACGCGACGATGGCT  420

Qy   2038 AAATGCGGTTGCCTCATTGGCCAAAGTTGTTGATCGAAACCGCCAGGTGATCGGCG 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAATGCGGTTGCCTCATTGGCCAAAGTTGTTGATCGAAACCGCCAGGTGATCGGCG  480

Qy   2098 ATGTGTGGGCCGGTGGTTTGGGCCATGCTCTGCGTGGGTGAGCTTCGCAC 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATGTGTGGGCCGGTGGTTTGGGCCATGCTCTGCGTGGGTGAGCTTCGCAC  540

Qy   2158 CAACTTCCCGCTGAAGGGCTGTGTGGTTTTAACAACAGTTCTTTGGGCCATGTGAAGTTGGAG 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CAACTTCCCGCTGAAGGGCTGTGTGGTTTTAACAACAGTTCTTTGGGCCATGTGAAGTTGGAG  600

Qy   2218 ATGCTCGGTCGTGGAGGGGACAGCCAGGAATTGGTACTGACCATGAGGAAGTGAAATTTCGCAGAG 2277
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ATGCTCGGTCGTGGAGGGGACAGCCAGGAATTGGTACTGACCATGAGGAAGTGAAATTTCGCAGAG  660
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RESULT 12
US-09-965-825-3
;   Sequence 3, Application US/09965825
;   Patent No. US20020150999A1
;   GENERAL INFORMATION:
;   FILE REFERENCE: 2135US0X
;   CURRENT APPLICATION NUMBER: US/09/965,825
;   CURRENT FILING DATE: 2001-10-01
;   PRIOR APPLICATION NUMBER: DE 10048604.5
;   PRIOR FILING DATE: 2000-09-30
;   PRIOR APPLICATION NUMBER: DE 10117085.8
;   PRIOR FILING DATE: 2001-04-06
;   APPLICANT: THIERBACH, Georg
;   APPLICANT: THOMAS, Hermann
;   APPLICANT: DUSCH, Nicole
;   TITLE OF INVENTION: CORYNEFORM BACTERIA
;   TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC ACID US
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 3
;   LENGTH: 875
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-965-825-3

Query Match      26.9%;    Score 875;   DB 9;     Length 875;
Best Local Similarity   100.0%;   Pred. No. 3.1e-270;
Matches  875;   Conservative     0;   Mismatches     0;   Indels     0;   Gaps     0;
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Qy   2278 ATTGCGGCGGCGCTGCCGGGTGTATCAAATCGTACCGCATCACCGATCCGAGAGAAGTTCGCCAG 2337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATTGCGGCGGCGCTGCCGGGTGTATCAAATCGTACCGCATCACCGATCCGAGAGAAGTTCGCCAG  720

Qy   2338 CAGCTAGCTGAGGCATTGGGCATATCCTGGACCCTGACTCTACTGATCGATATCGTCACGGATCCT 2397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGCTAGCTGAGGCATTGGGCATATCCTGGACCCTGACTCTACTGATCGATATCGTCACGGATCCT  780

Qy   2398 AATGGCGCTGTCGATCCCACCAACCATCACGTGGGGACAGGTCATGGGAATTCAGCAAGGCG 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AATGGCGCTGTCGATCCCACCAACCATCACGTGGGGACAGGTCATGGGAATTCAGCAAGGCG  840

Qy   2458 GCCACCCGGAACCGTCTCTTTGGTGGGAGGAGTAGGAGTAGGAGCCGATGATCTGGCCCGGTTCGAAC 2517
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCCACCCGGAACCGTCTCTTTGGTGGGAGGAGTAGGAGTAGGAGCCGATGATCTGGCCCGGTTCGAAC  900

Qy   2518 ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT 2561
          ||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATAAGGAATATTCCTACTCCATGATGATTGATACACCTGCTGTT  944
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Qy   1180 TGCGAGATGGTGAAATGGTGGTTGAGCAGGGTGAAACGCATTTTGCATCACGGCATTCAGTCC 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGCGAGATGGTGAAATGGTGGTTGAGCAGGGTGAAACGCATTTTGCATCACGGCATTCAGTCC   60

Qy   1240 ACCATGGCGGGGTAAAGGTGTGTCGGGTGGTAGTGAATTCCTGGTGGTTGATTGCTAAGGAAGAC 1299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCATGGCGGGGTAAAGGTGTGTCGGGTGGTAGTGAATTCCTGGTGGTTGATTGCTAAGGAAGAC  120

Qy   1300 GCAGGTGCACGGTGACTTATTCCACTATTTCTTCTGGCCACTCCTGTGTTGTTCCCG 1359
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCAGGTGCACGGTGACTTATTCCACTATTTCTTCTGGCCACTCCTGTGTTGTTCCCG  180

Qy   1360 GATCCTACTGAGGCGTCCAGCCCGTGGAGACGGATTAAACAGCTAAGTCNGTCACTTTG 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATCCTACTGAGGCGTCCAGCCCGTGGAGACGGATTAAACAGCTAAGTCNGTCACTTTG  240

Qy   1420 TTCTGCGGTGCGGGCGTGAAGAAATGCTCGGCGGTTGGAGTTGGCGGGAGAGATT 1479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTCTGCGGTGCGGGCGTGAAGAAATGCTCGGCGGTTGGAGTTGGCGGGAGAGATT  300

Qy   1480 AAATCACCGACTCGGGCATGCGCCTGGGGTGGTAAGCAGTACATCCAGCATGAGAATCCGTTT 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480
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RESULT 13
US-10-143-856-5
; Sequence 5, Application US/10143856
; Publication No. US20030109014A1
; GENERAL INFORMATION:
; APPLICANT: BURKE, KEVIN
; APPLICANT: DUNICAN, L.K.
; APPLICANT: McCORMACK, ASHLING
; APPLICANT: STAPLETON, CLIONA
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: Process for the fermentative preparation of
; TITLE OF INVENTION: with amplification of the tkt gene
; FILE REFERENCE: MAS/021123/282432
; CURRENT APPLICATION NUMBER: US/10/143,856
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/986,649
; PRIOR FILING DATE: 17-03-2000
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-143-856-5

Query Match   26.9%; Score 875; DB 15; Length 875;
Best Local Similarity 100.0%; Pred. No. 3.1e-270;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1180 TCGGAGAAGGGTGAATGGTGGTGAGCAGGGTGAAGCGATTCAGTCC 1239
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Db   1 TCGGAGAAGGGTGAATGGTGGTGAGCAGGGTGAAGCGATTCAGTCC 60

RESULT 14
US-10-078-167-6
; Sequence 6, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
; APPLICANT: Dunican, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona
; APPLICANT: Mockel, Bettina
; APPLICANT: Burke, Kevin
; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; TITLE OF INVENTION: a gene encoding 6-Phosphogluconate Dehydrogenase
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/078,167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16

RESULT 15

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-078-167-6

Query Match 26.9%; Score 875; DB 15; Length 875;
Best Local Similarity 100.0%; Pred. No. 3.1e-270;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1180 TGCGAGATGGTGAATGGGTGGTGAGCAGGGTGAACGGCATTTTGCATCACGGCGATTCAGTCC 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGCGAGATGGTGAATGGGTGGTGAGCAGGGTGAACGGCATTTTGCATCACGGCGATTCAGTCC 60

Qy   1240 ACCATGGCGGGGTAAAGGTGTGGTGGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGAC 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCATGGCGGGGTAAAGGTGTGGTGGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGAC 120

Qy   1300 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 180

Qy   1360 GATCCTACTGAGGCTGGAGACGCGCTCGGTCGGGAGCAGTTAACAACGCTAAGTCTCACTTTG 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATCCTACTGAGGCTGGAGACGCGCTCGGTCGGGAGCAGTTAACAACGCTAAGTCTCACTTTG 240

Qy   1420 TTCTCGCGGTGCGGGGGGGTGAAGAATGCTCGCCGCGCACGTGTTGGGCGGCGAGAGAT 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTCTCGCGGTGCGGGGGGGTGAAGAATGCTCGCCGCGCACGTGTTGGGCGGCGAGAGAT 300

Qy   1480 AAATCACCGATCGGCGCATGCGGCTGGGTAGTGGTGGTTAAGCAGTACAATCCAGCATGAGAATCCGGTT 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAATCACCGATCGGCGCATGCGGCTGGGTAGTGGTGGTTAAGCAGTACAATCCAGCATGAGAATCCGGTT 360

Qy   1540 GAGGTCGGCAGTCTCGGCCTTGGTTAGGCGGCCCTGGGTGAGATGCGTCCAATGAGGCG 1599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGTCGGCAGTCTCGGCCTTGGTTAGGCGGCCCTGGGTGAGATGCGTCCAATGAGGCG 420

Qy   1600 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 480

Qy   1660 GTTGCCCAGGTGGAATATCAAGCGGTCGCGCACATTGCCTGACGGTACCAGGGTGAAGTATCCG 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTTGCCCAGGTGGAATATCAAGCGGTCGCGCACATTGCCTGACGGTACCAGGGTGAAGTATCCG 540

Qy   1720 GTGACCGGTGAGTTGCTGCAACAATCGAAAAATATTTTGCCTCATGTGAAGGAAGAAAAACA 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGACCGGTGAGTTGCTGCAACAATCGAAAAATATTTTGCCTCATGTGAAGGAAGAAAAACA 600

Qy   1780 GATCGTTTCCTTCCTTGATCGGATCGGATTCGGAGCTCGGTGGTA 1839
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GATCGTTTCCTTCCTTGATCGGATCGGATTCGGAGCTCGGTGGTA 660

Qy   1840 GAGACGTACACATAAACGTCGACAGCAATACGTTGCCTCT 1899
          ||||||||||||||||||||||||||||||||||||||||
Db    661 GAGACGTACACATAAACGTCGACAGCAATACGTTGCCTCT 720

Qy   1900 ATTTTGAACGAGCTGGCGGATAAGAGTGCGGTGTTACTCTGGATACCGGCAAT 1959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTTTGAACGAGCTGGCGGATAAGAGTGCGGTGTTACTCTGGATACCGGCAAT 780

Qy   1960 GTGTGCATGCGAGGTACATCGAGAATCCCGAGGAAACGCGCGACTTTGTGGGTTCATTC 2019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGTGCATGCGAGGTACATCGAGAATCCCGAGGAAACGCGCGACTTTGTGGGTTCATTC 840

Qy   2020 CGCCACGGCACGATGGGCTAAATGCGTTGCCTCATGC 2054
          |||||||||||||||||||||||||||||||||||||
Db    841 CGCCACGGCACGATGGGCTAAATGCGTTGCCTCATGC 875
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US-10-336-049-6
; Sequence 6, Application US/10336049
; Publication No. US20030127591A1
; GENERAL INFORMATION:
; FILE REFERENCE: 7601/80158
; CURRENT APPLICATION NUMBER: US/10/336,049
; CURRENT FILING DATE: 2003-01-30
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 6
; TITLE OF INVENTION: the zwf Gene
; TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification o
; APPLICANT: Mockel, Bettina
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Thierbach, Georg
; APPLICANT: Reth, Alexander
; APPLICANT: Bathe, Brigitte
; APPLICANT: Hans, Stephan
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-10-336-049-6

Query Match 26.9%; Score 875; DB 15; Length 875;
Best Local Similarity 100.0%; Pred. No. 3.1e-270;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1180 TGCGAGATGGTGAATGGGTGGTGAGCAGGGTGAACGGCATTTTGCATCACGGCGATTCAGTCC 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGCGAGATGGTGAATGGGTGGTGAGCAGGGTGAACGGCATTTTGCATCACGGCGATTCAGTCC 60

Qy   1240 ACCATGGCGGGGTAAAGGTGTGGTGGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGAC 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCATGGCGGGGTAAAGGTGTGGTGGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGAC 120

Qy   1300 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 180

Qy   1360 GATCCTACTGAGGCTGGAGGCTGCAGCCCGTGGTGGACGGATTAACAACGCTAAGTCTCACTTTG 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAATCACCGATCGGCGCATGCGGCTGGGTAGTGGTGGTTAAGCAGTACAATCCAGCATGAGAATCCGGTT 240

Qy   1420 TTCTCGCGGTGCGGGGGGGTGAAGAATGCTCGCCGCGCACGTGTTGGGCGGCGAGAGAT 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATCCTACTGAGGCTGGAGGCTGCAGCCCGTGGTGGACGGATTAACAACGCTAAGTCTCACTTTG 240

Qy   1300 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCAGGTGACGGTACTTATTCCAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 180

Qy   1240 ACCATGGCGGGGTAAAGGTGTGGTGGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGAC 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCATGGCGGGGTAAAGGTGTGGTGGGTAGTGATTCCTGGTGATATCGGCTAAGGAAGAC 120

Qy   1480 AAATCACCGATCGGCGCATGCGGCTGGGTAGTGGTGGTTAAGCAGTACAATCCAGCATGAGAATCCGGTT 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAATCACCGATCGGCGCATGCGGCTGGGTAGTGGTGGTTAAGCAGTACAATCCAGCATGAGAATCCGGTT 360

Qy   1360 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 180

Qy   1540 GAGGTCGGCAGTCTCGGCCTTGGTTAGGCGGCCCTGGGTGAGATGCGTCCAATGAGGCG 1599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAATCACCGATCGGCGCATGCGGCTGGGTAGTGGTGGTTAAGCAGTACAATCCAGCATGAGAATCCGGTT 360

Qy   1480 GCAGGTGACGGTACTTATTCAAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCAGGTGACGGTACTTATTCAAATTCCACTATTTCTTCTGGCACTCCTGTGGTGTTCCCG 240

Qy   1420 TTCTCGCGGTGCGGGGGGGTGAAGAATGCTCGCCGCGCACGTGTTGGGCGGCGAGAGAT 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTCTCGCGGTGCGGGGGGGTGAAGAATGCTCGCCGCGCACGTGTTGGGCGGCGAGAGAT 300

Qy   1600 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 480

Qy   1780 GTTGCCCAGGTGGAATATCAACGGTCGCGCACATTGCCTGACGGTACCAGGGTGAAGTATCCG 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTTGCCCAGGTGGAATATCAACGGTCGCGCACATTGCCTGACGGTACCAGGGTGAAGTATCCG 540

Qy   1660 GTTGCCCAGGTGGAATATCAAGCGGTCGCGCACATTGCCTGACGGTACCAGGGTGAAGTATCCG 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGACCGGTGAGTTGCTGCAACAATCGAAAAATATTTTGCCTCATGTGAAGGAAGAAAAACA 600

Qy   1720 GTGACCGGTGAGTTGCTGCAACAATCGAAAAATATTTTGCCTCATGTGAAGGAAGAAAAACA 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GATCTGCTGATTCTATTGGGGTACGGATTTCCCTTATTCTGATTTTCCTTCCTAAAGACAAC 480

Qy   1840 GAGACGTACACATAAACGTCGACAGCAATACGTTGCCTCT 1899
          ||||||||||||||||||||||||||||||||||||||||
Db    601 GATCGTTTCCTTCCTTGATCGGATCGGATTCGGAGCTCGGTGGTA 660
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Db    661  GAGACGTACACATAAGGTCGAGAAGCATGTGCCTATTCACCCTGAATACGTTGCCTCT 720

Qy   1900  ATTTTGAACGAGCTGGCGGGATAAGGATGCGGGTGTTTACTGTGGGATACCGGCATGTGCAAT 1959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATTTTGAACGAGCTGGCGGGATAAGGATGCGGGTGTTTACTGTGGGATACCGGCATGTGCAAT 780

Qy   1960  GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 2019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GTGTGGCATGCGAGGTACATCGAGAATCCGGAGGGAACGCGCGACTTTGTGGGTTCATTC 840

Qy   2020  CGCCACGGCACGATGGGCTAAATGCGTTGCCTCATGC 2054
           ||||||||||||||||||||||||||||||||||||
Db    841  CGCCACGGCACGATGGGCTAAATGCGTTGCCTCATGC 875
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